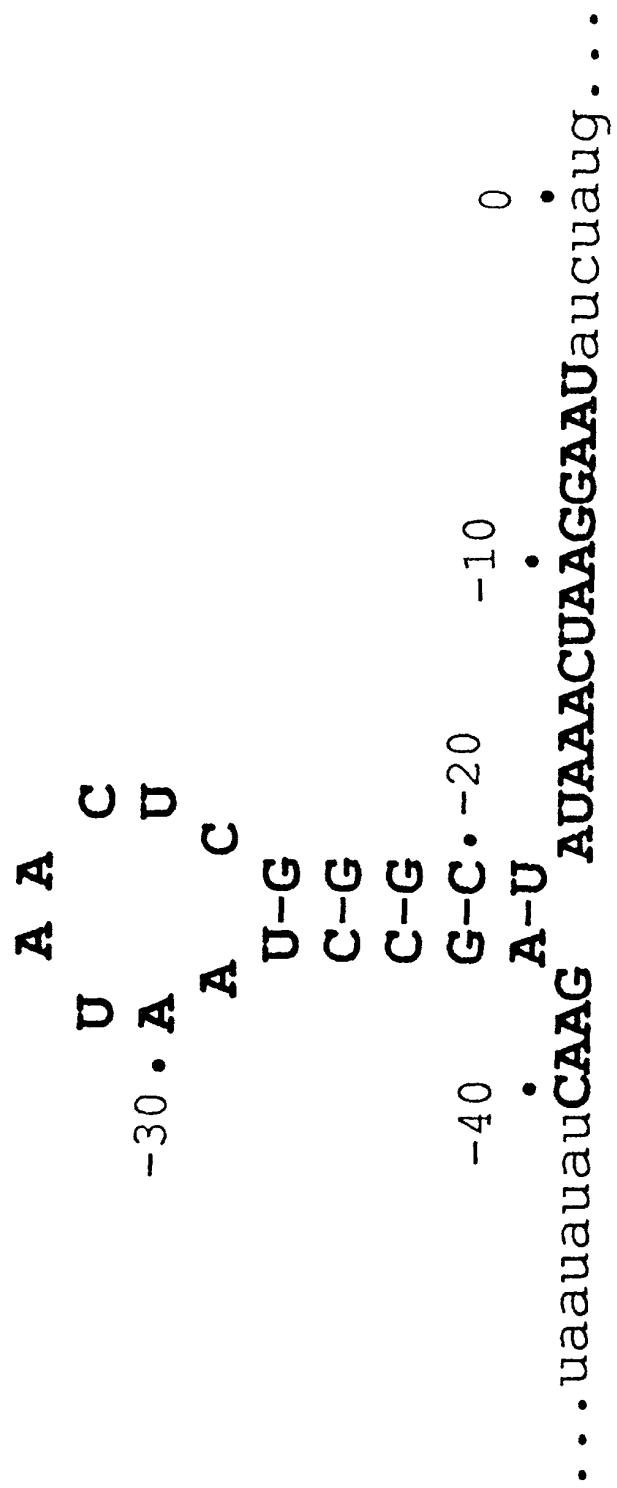


FIG. I



SEQ. I.D. NO. 345

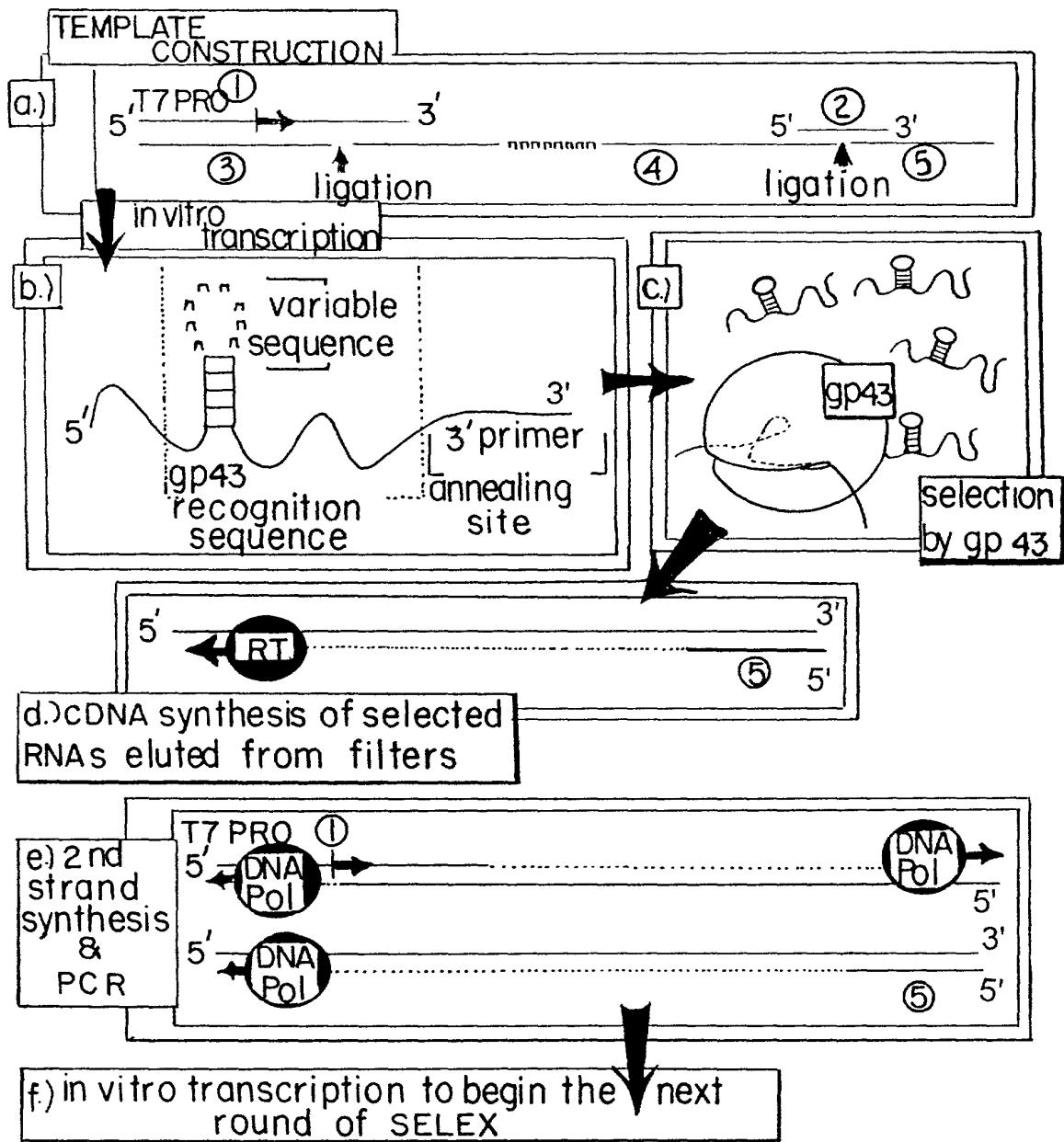


FIG.2

FIG.3

SELECTION CYCLE:

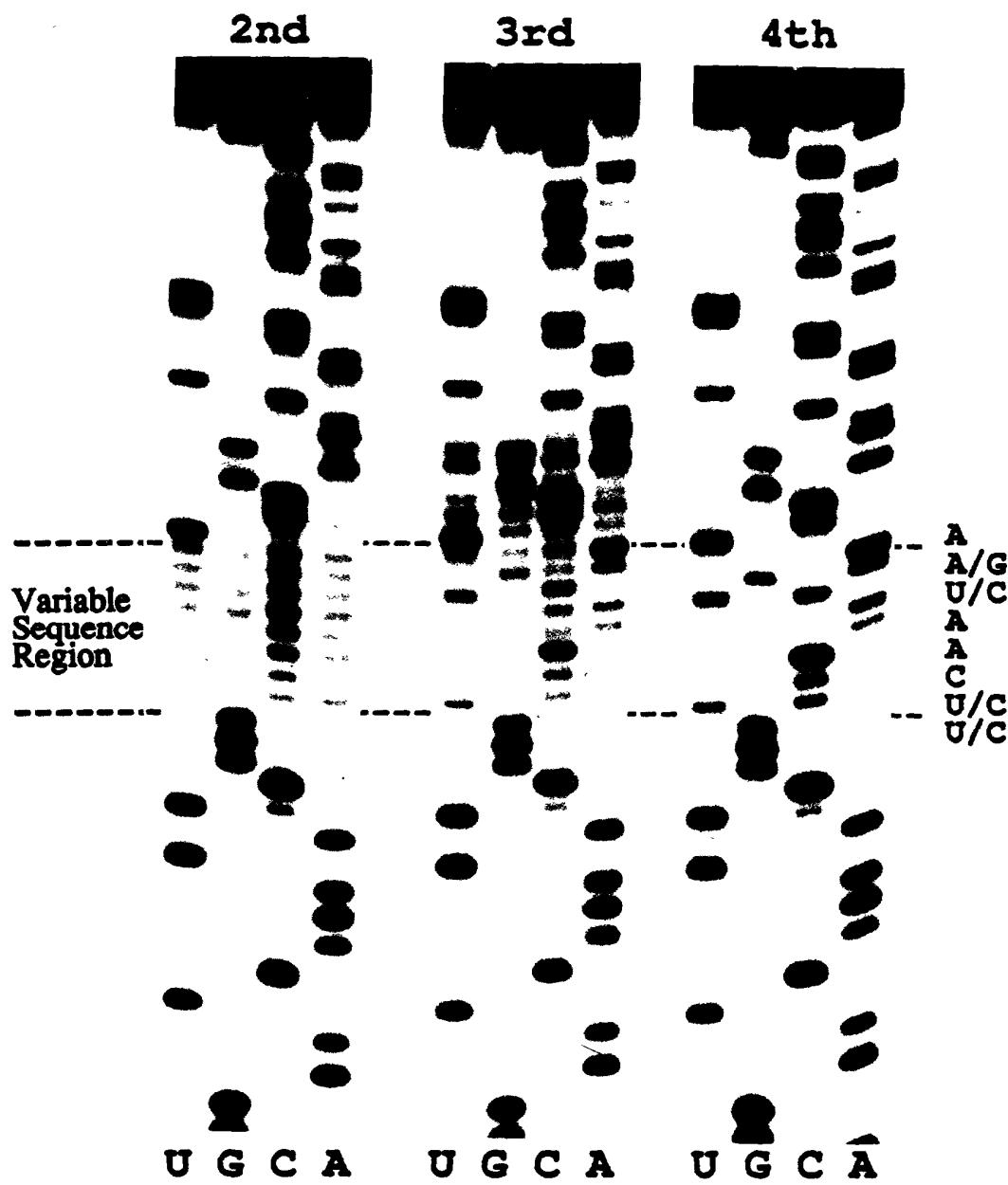


FIG.4

EXPERIMENT:

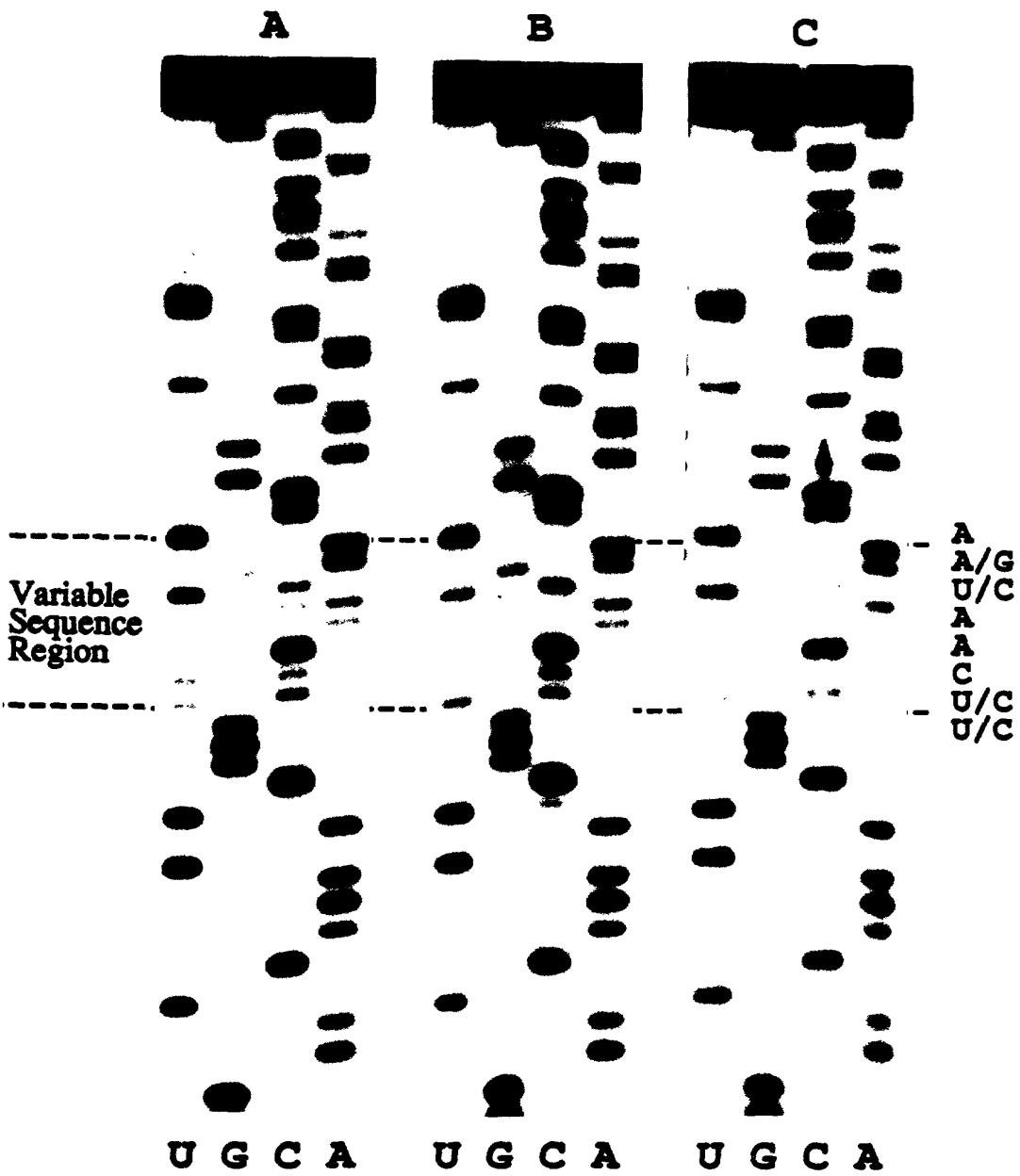


FIG. 5

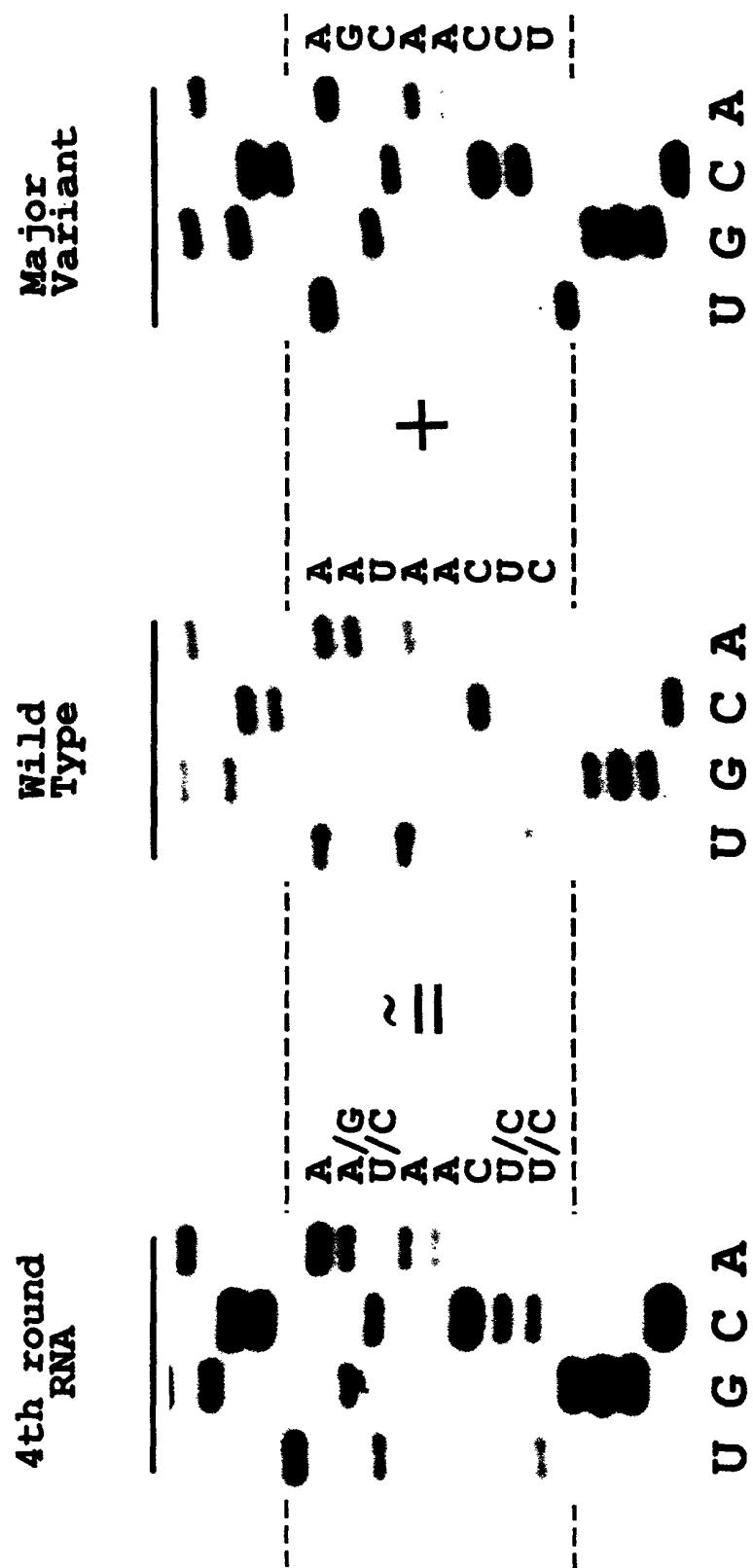
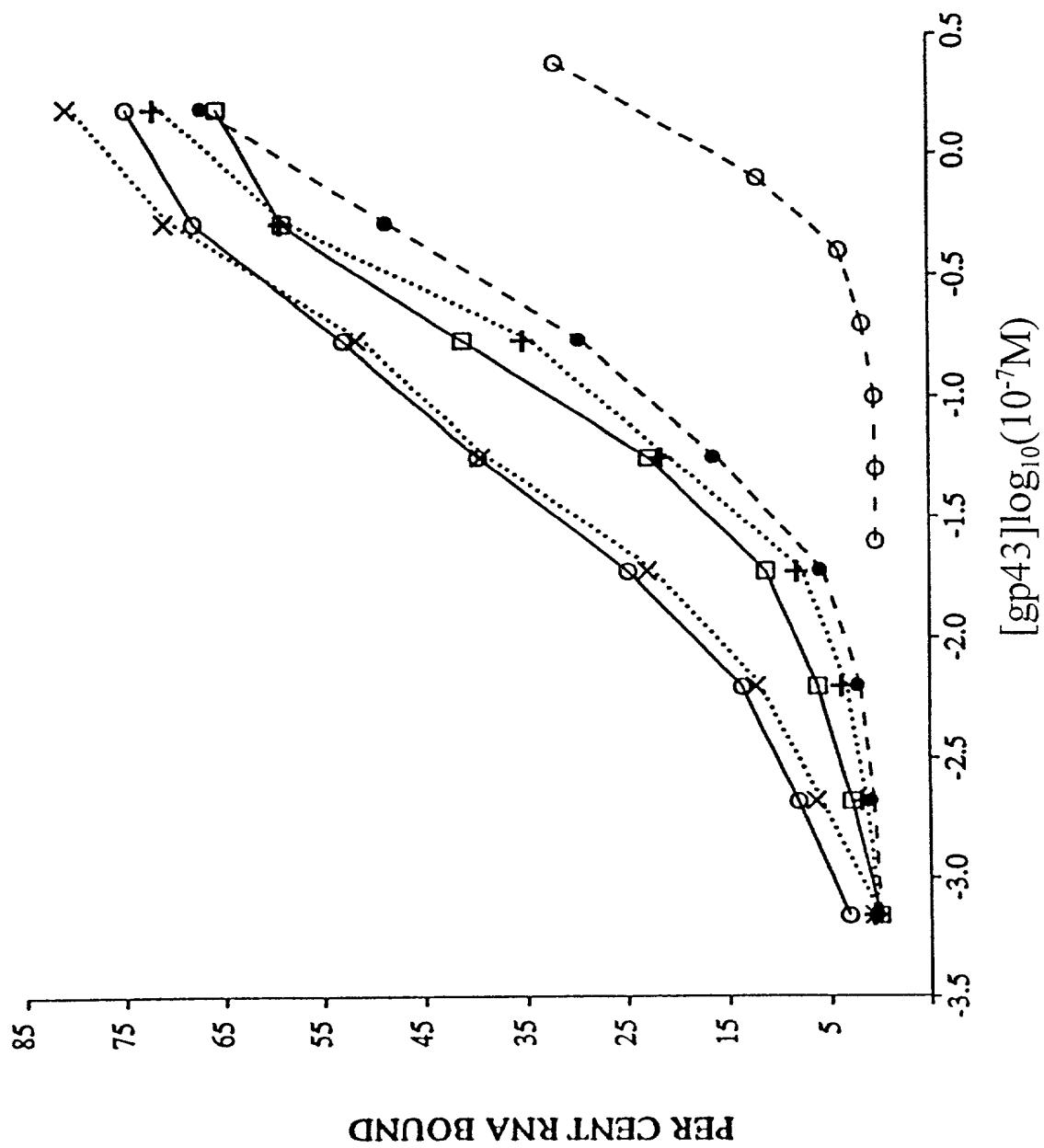


FIG. 6



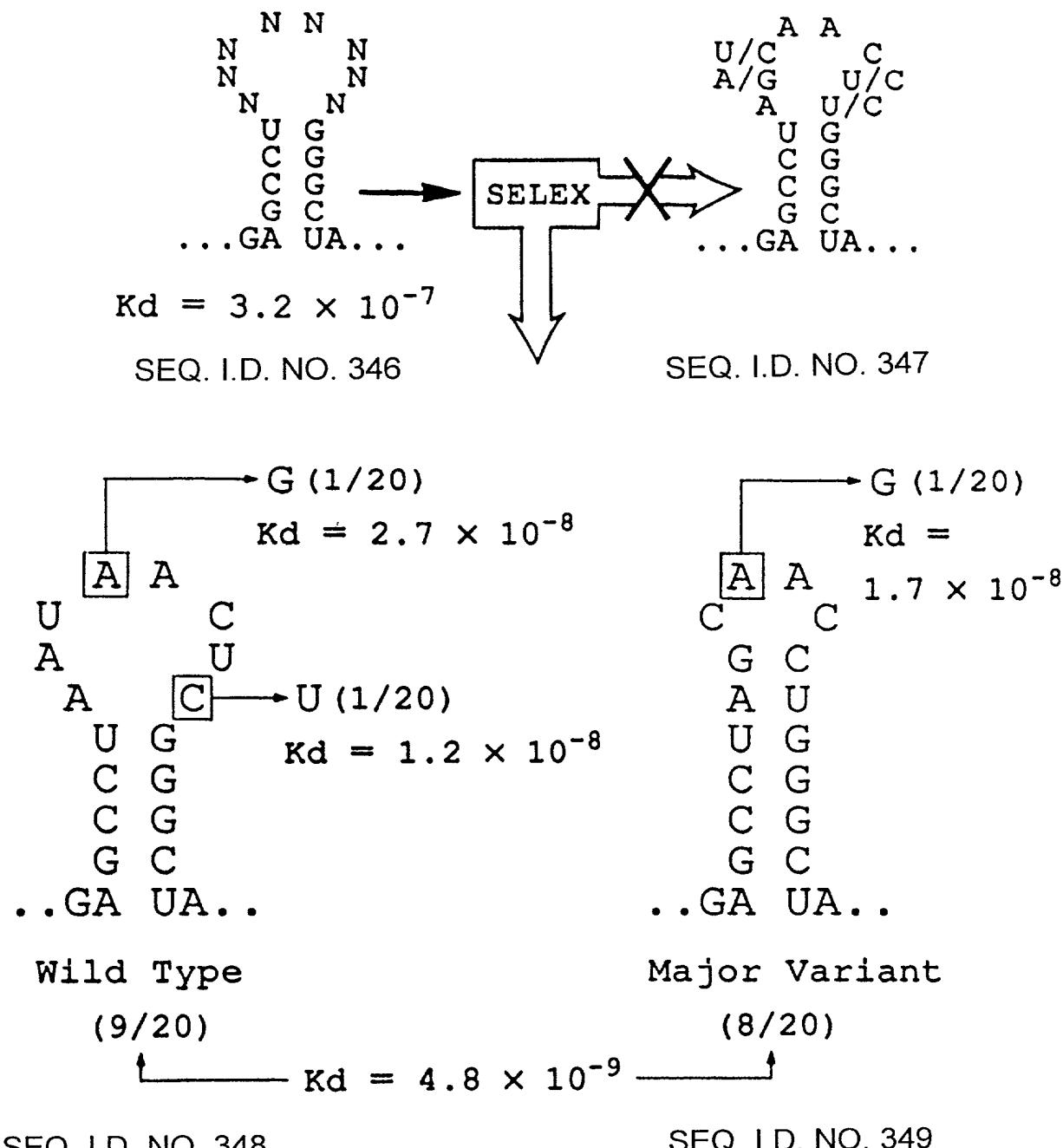
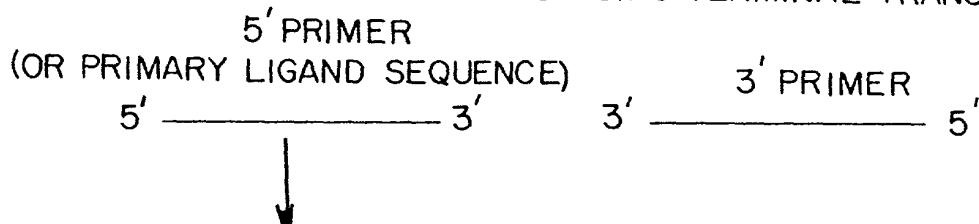


FIG. 7

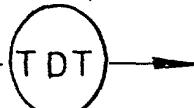
VARIABLE TEMPLATE SYNTHESIS USING TERMINAL TRANSFERASE



TAILING WITH TERMINAL TRANSFERASE  
USING RANDOM NUCLEOTIDES.

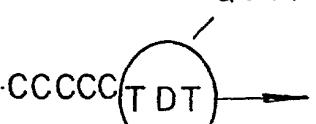
5'

dNTPs



HOMOPOLYMER TAILING OF LENGTHENED 5'  
PRIMER & 3' PRIMER.

5'



3' PRIMER

ANNEALING & FILLIN

5'



CCCCC  
G GGGGG

FIG. 8

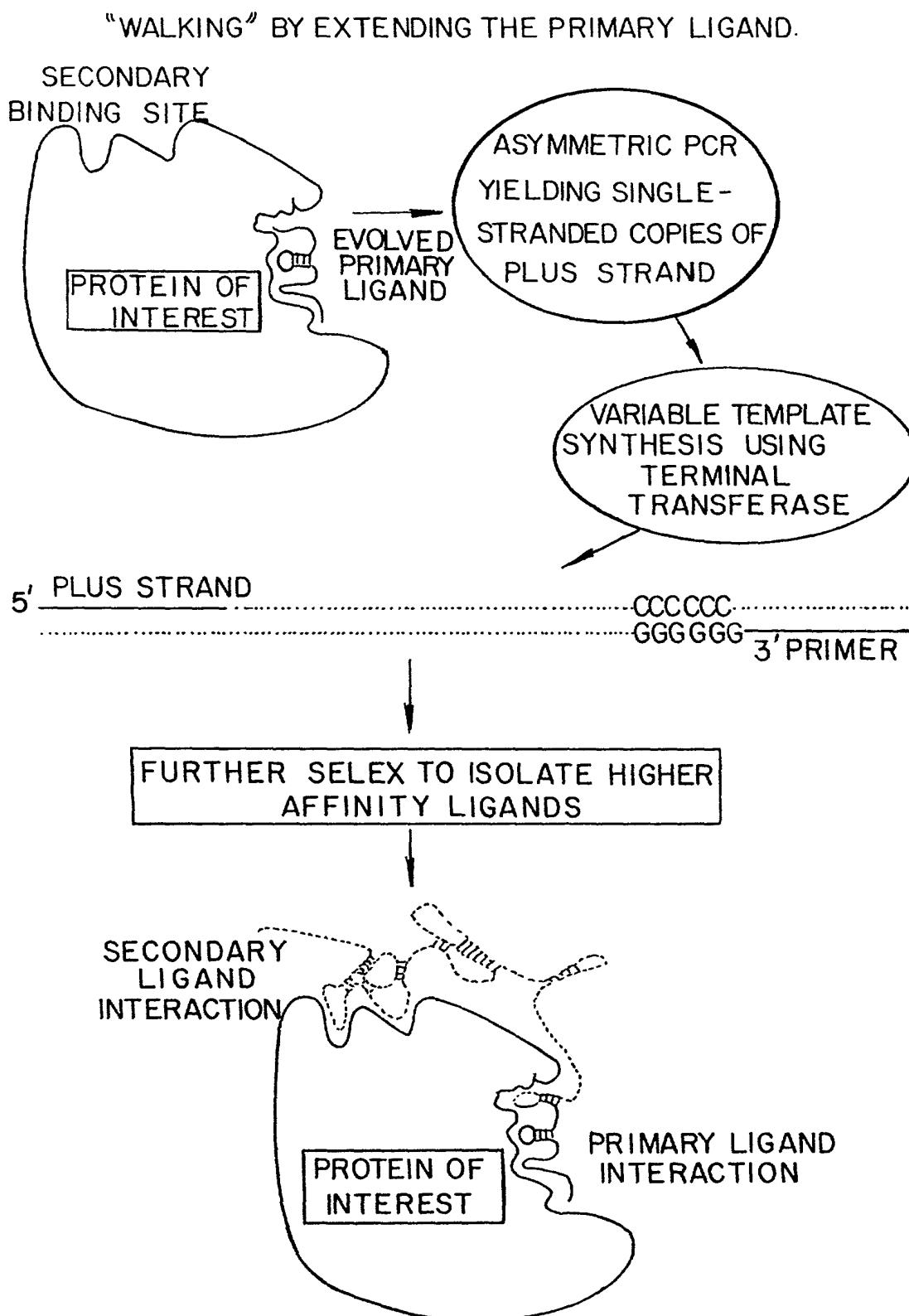


FIG. 9

ANCHORING OF BRIDGING OLIGONUCLEOTIDE &  
SECONDARY LIGAND EVOLUTION.

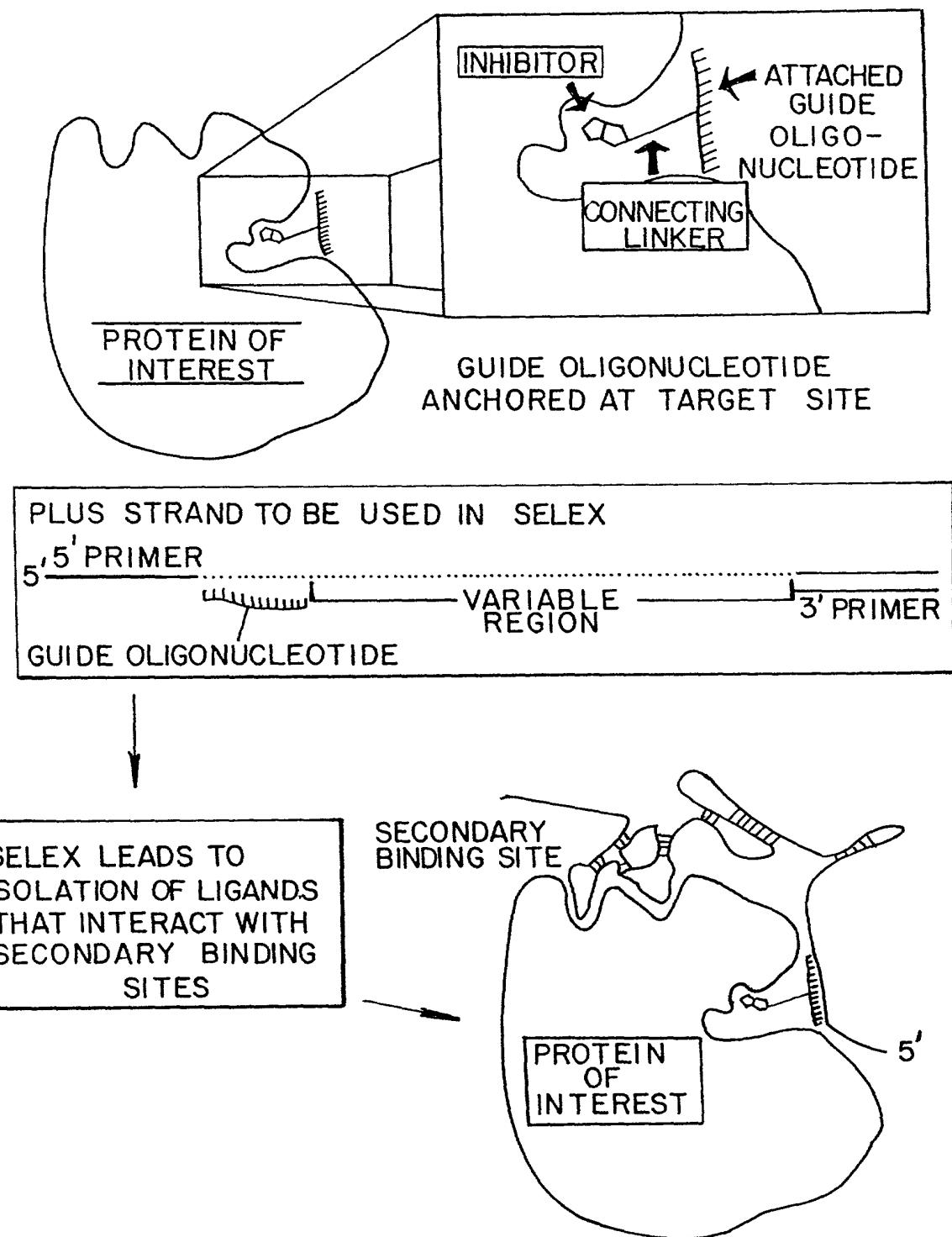


FIG.10

SECONDARY LIGAND-DIRECTED PRIMARY LIGAND EVOLUTION.

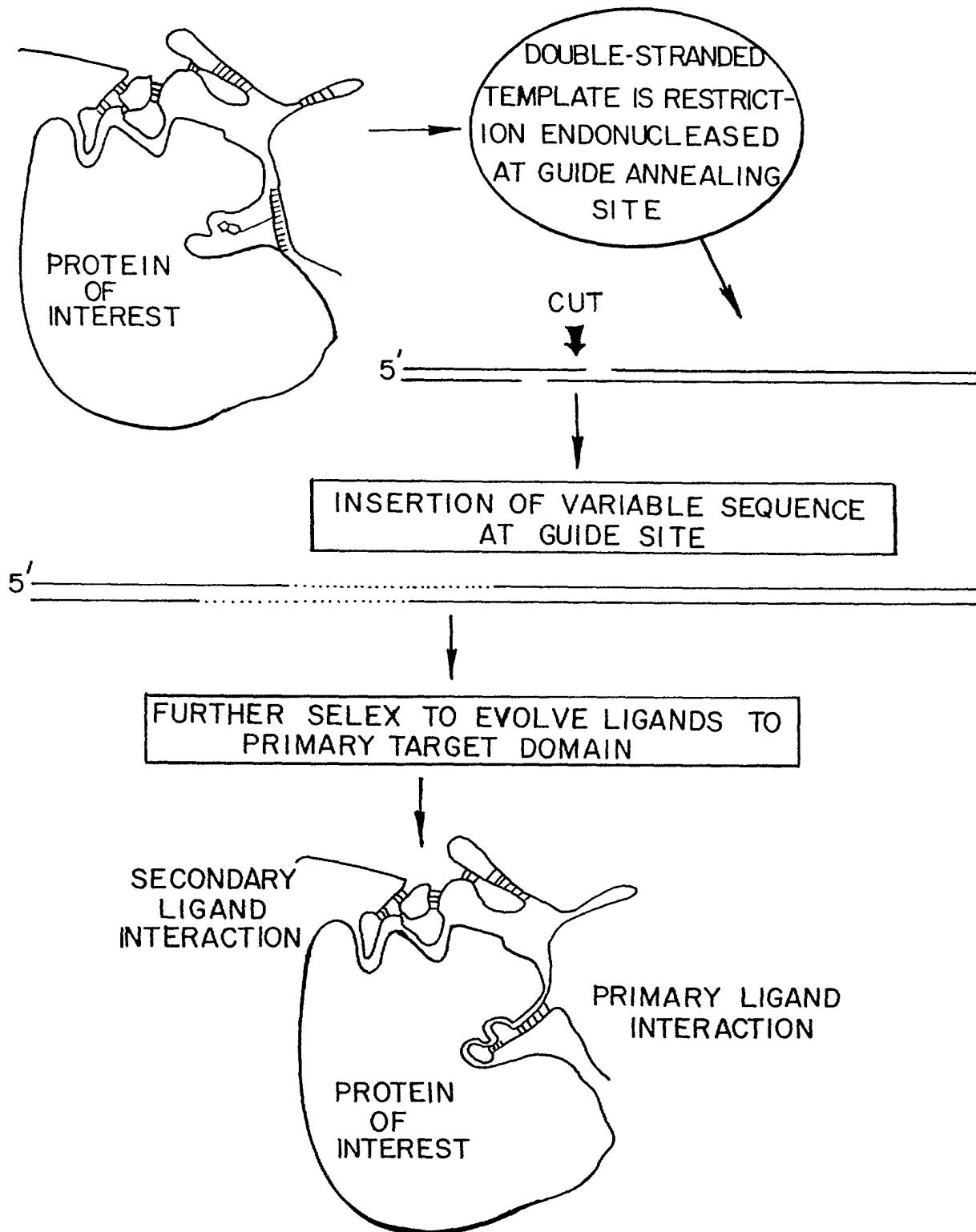
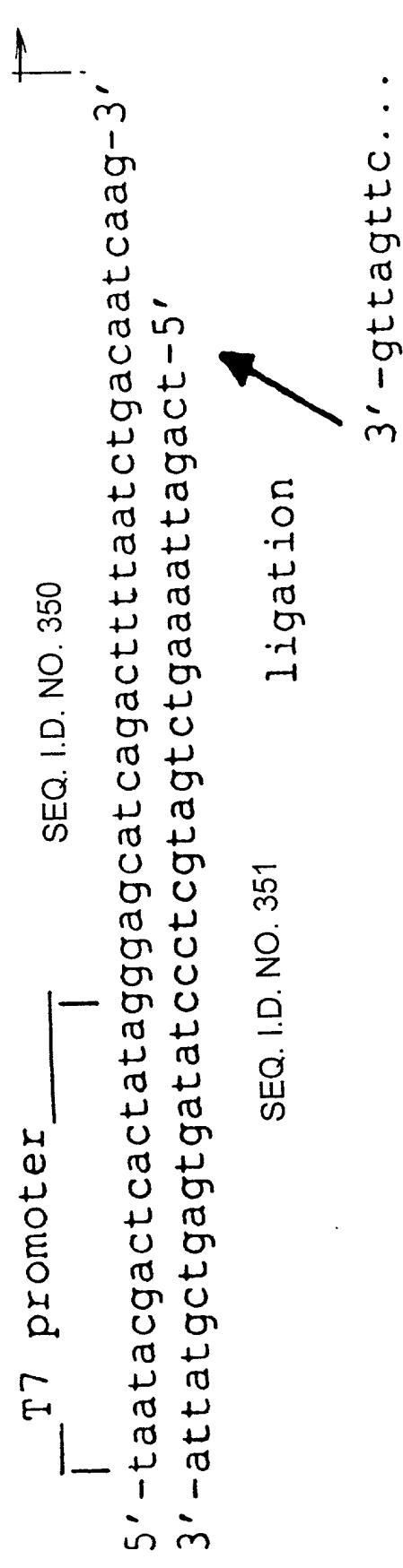


FIG.11



in vitro transcript

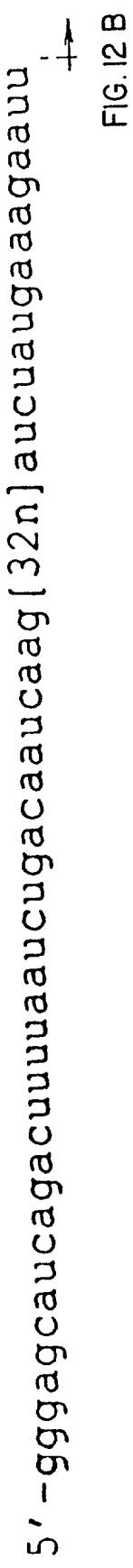
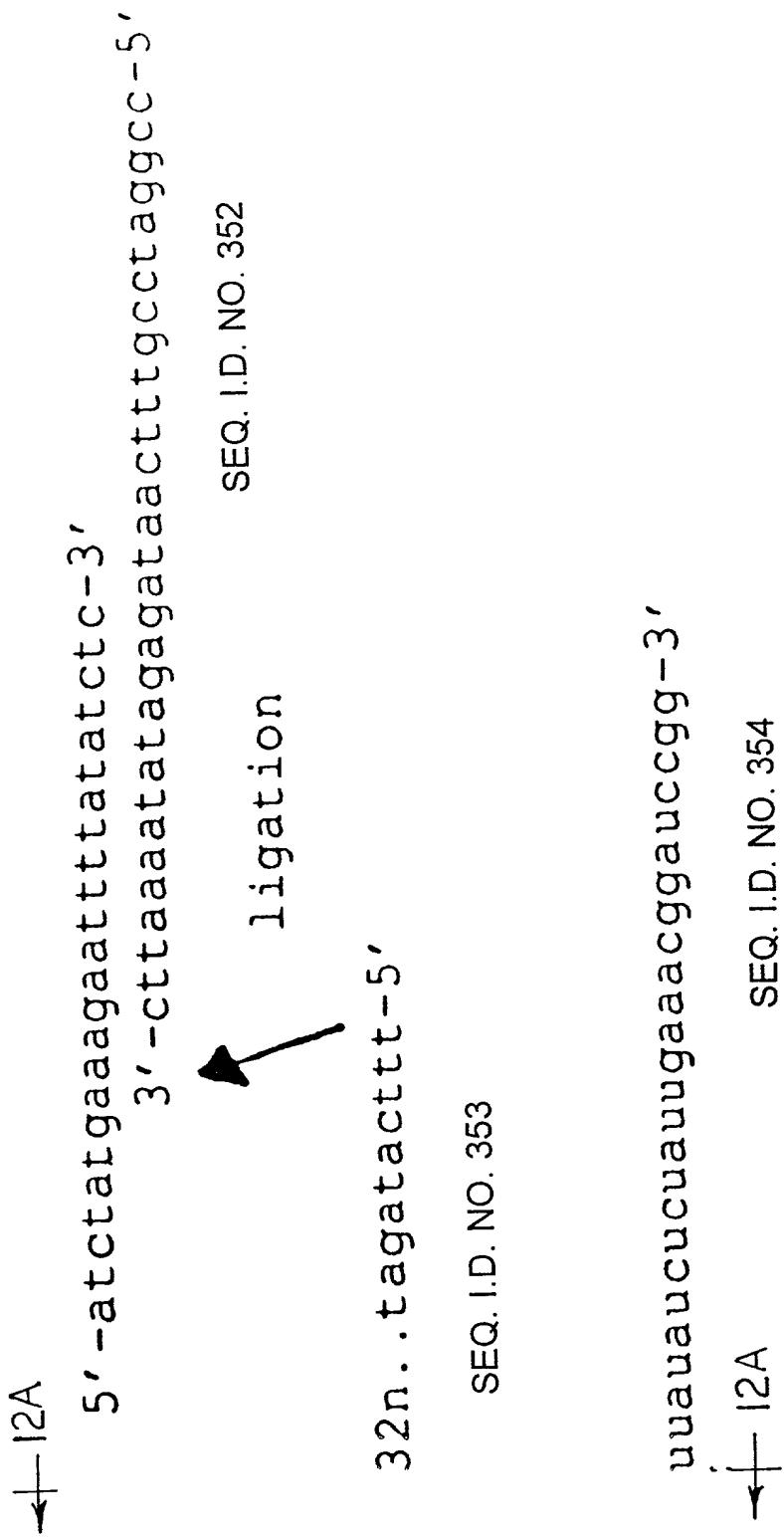


FIG.12 A



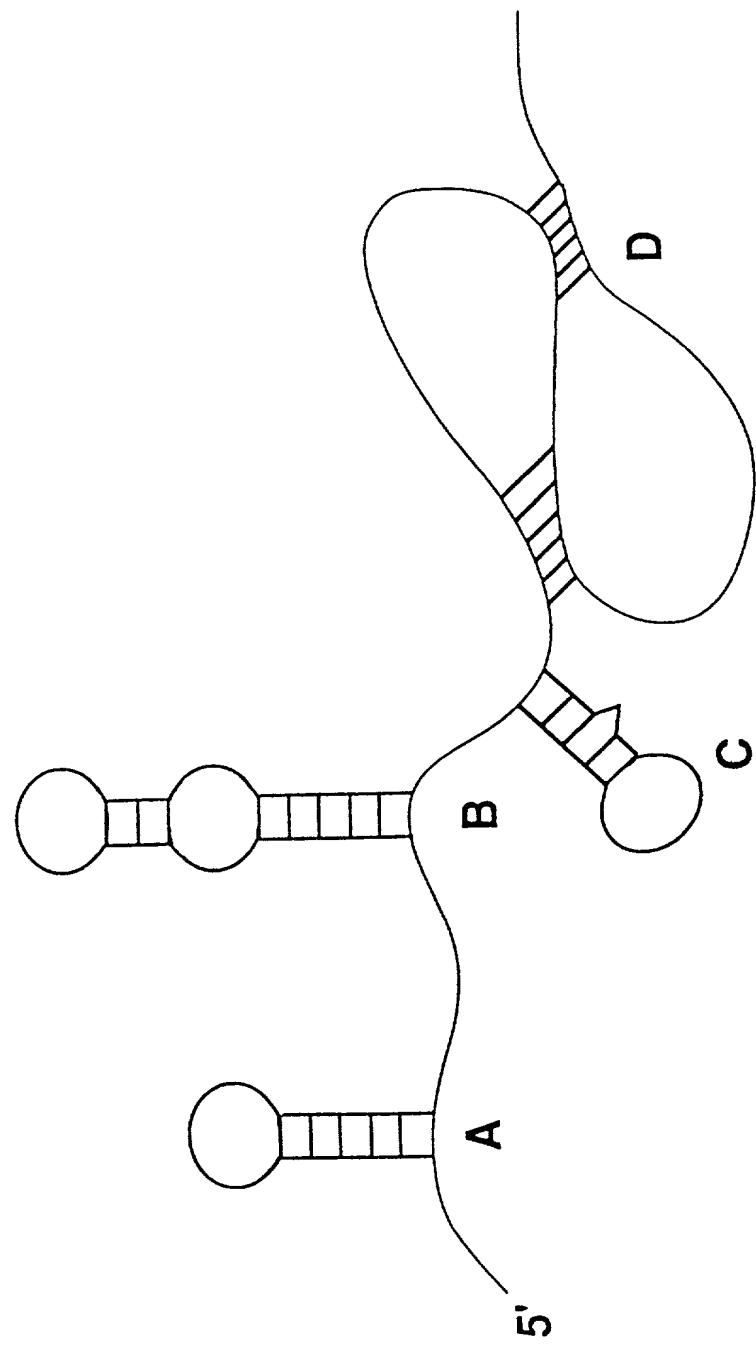
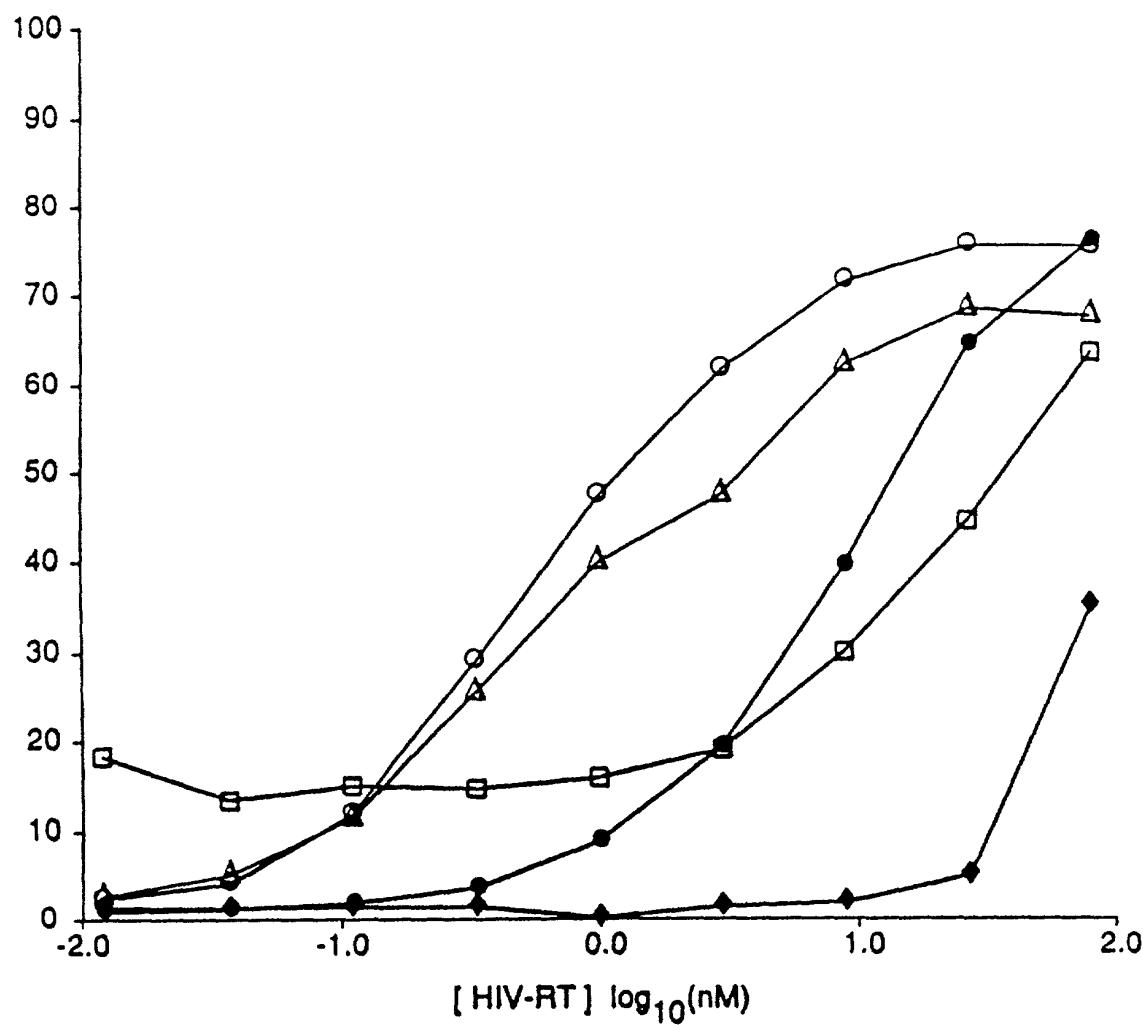


FIG. 13

FIG.14



△ 1.1 ucaagAAUUCCCGUUUUCAGUCGGGAAAAACUGAACAaucu (13)

○ 1.3 ucaagAAUAUCUCCGAAGCCGAACGGGAAAACCCGGCaucu (1)

● 1.3 ----- G ----- A ----- (1)

□ 1.4 ucaagGGCAUCUGGGAGGGUAAGGGUAAGGUUGUCGGaucu (4)

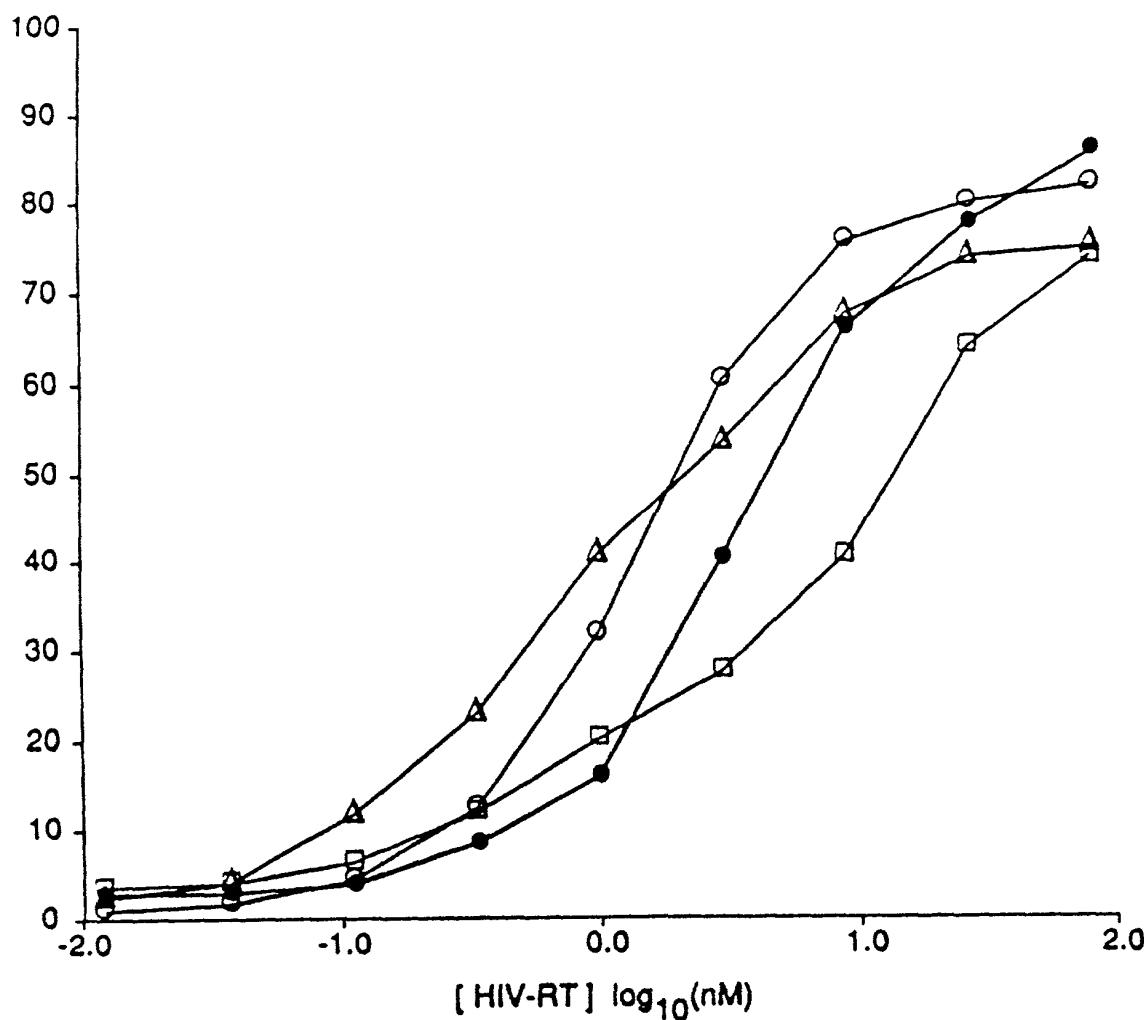
△ 1.1 = SEQ. I.D. NO. 355

● 1.3 = SEQ. I.D. NO. 357

○ 1.3 = SEQ. I.D. NO. 356

□ 1.4 = SEQ. I.D. NO. 358

FIG. 15



ISOLATE

○ 2.1 a ucaag--AAUAUA-UCCGAACCUCGACGGGAUAACGAGAA-Gaucu (3)

□ 2.2 b ucaagUACCUAGGUAAAAGGGAGAACACGUGUGUU-cu (13)

● 2.5 b ucaagACAGUAUCCGUUCUUGAUCACGGGACAAAUGaucu (3)

△ 1.1 ucaagAAUCCGUUUUCAGUCGGAAAAACUGAACAucu (13)

○ 2.1a = SEQ. I.D. NO. 359

● 2.5b = SEQ. I.D. NO. 361

□ 2.2b = SEQ. I.D. NO. 360

△ 1.1 = SEQ. I.D. NO. 362

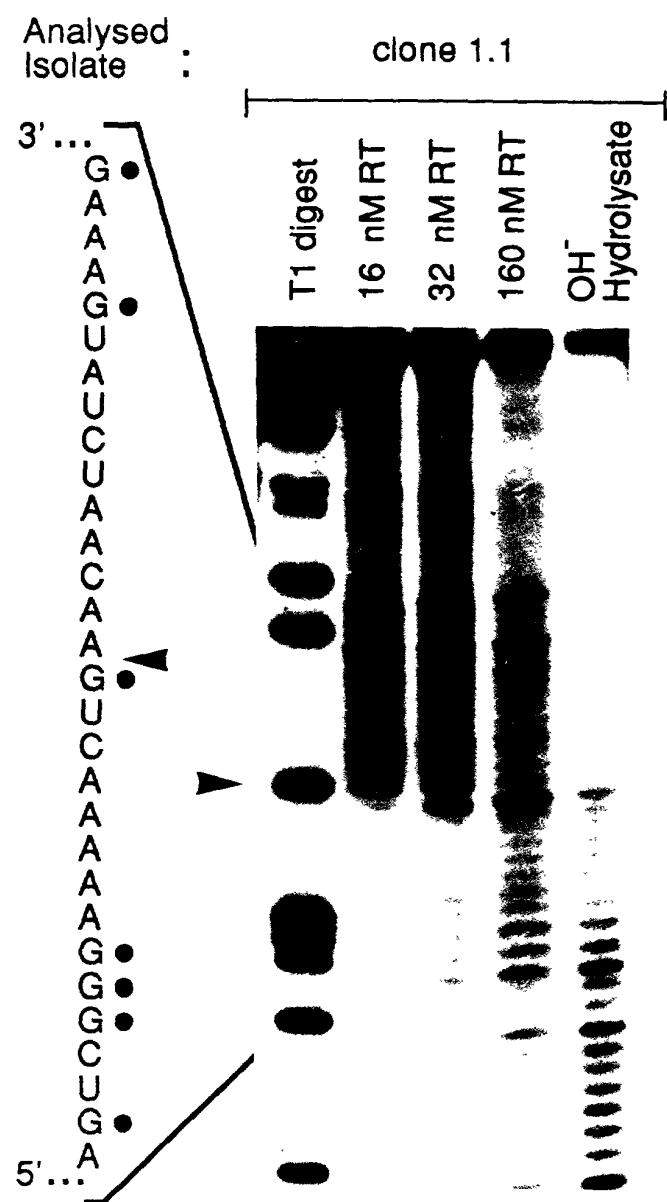


FIG. 16 A

SEQ. I.D. NO. 363

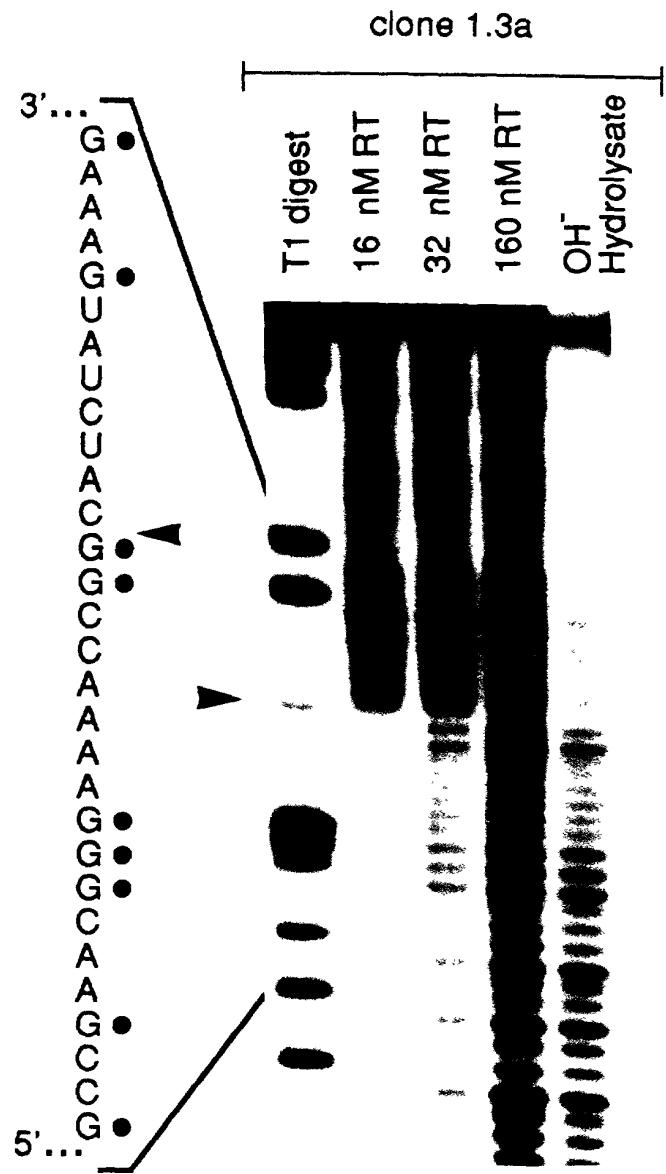
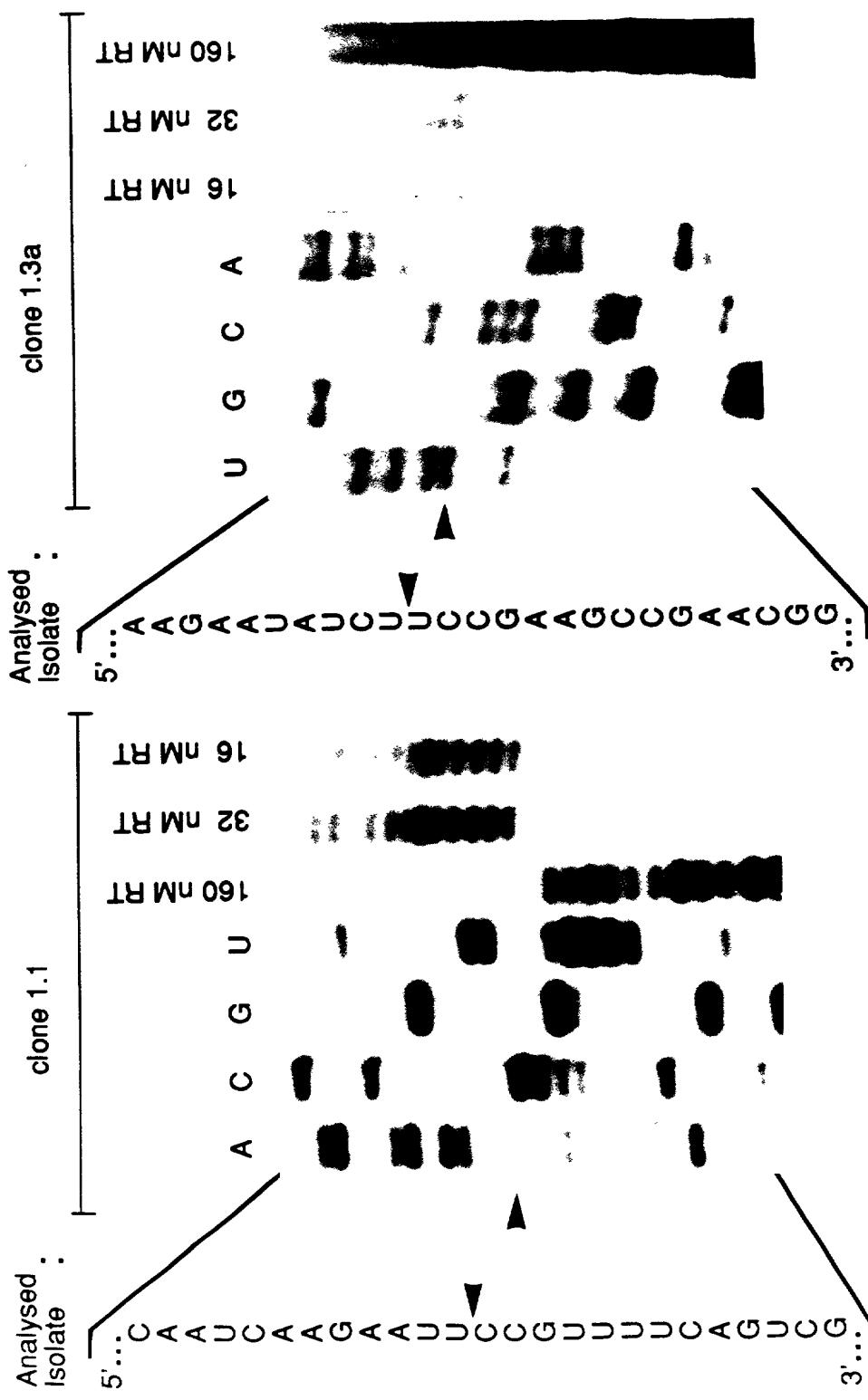
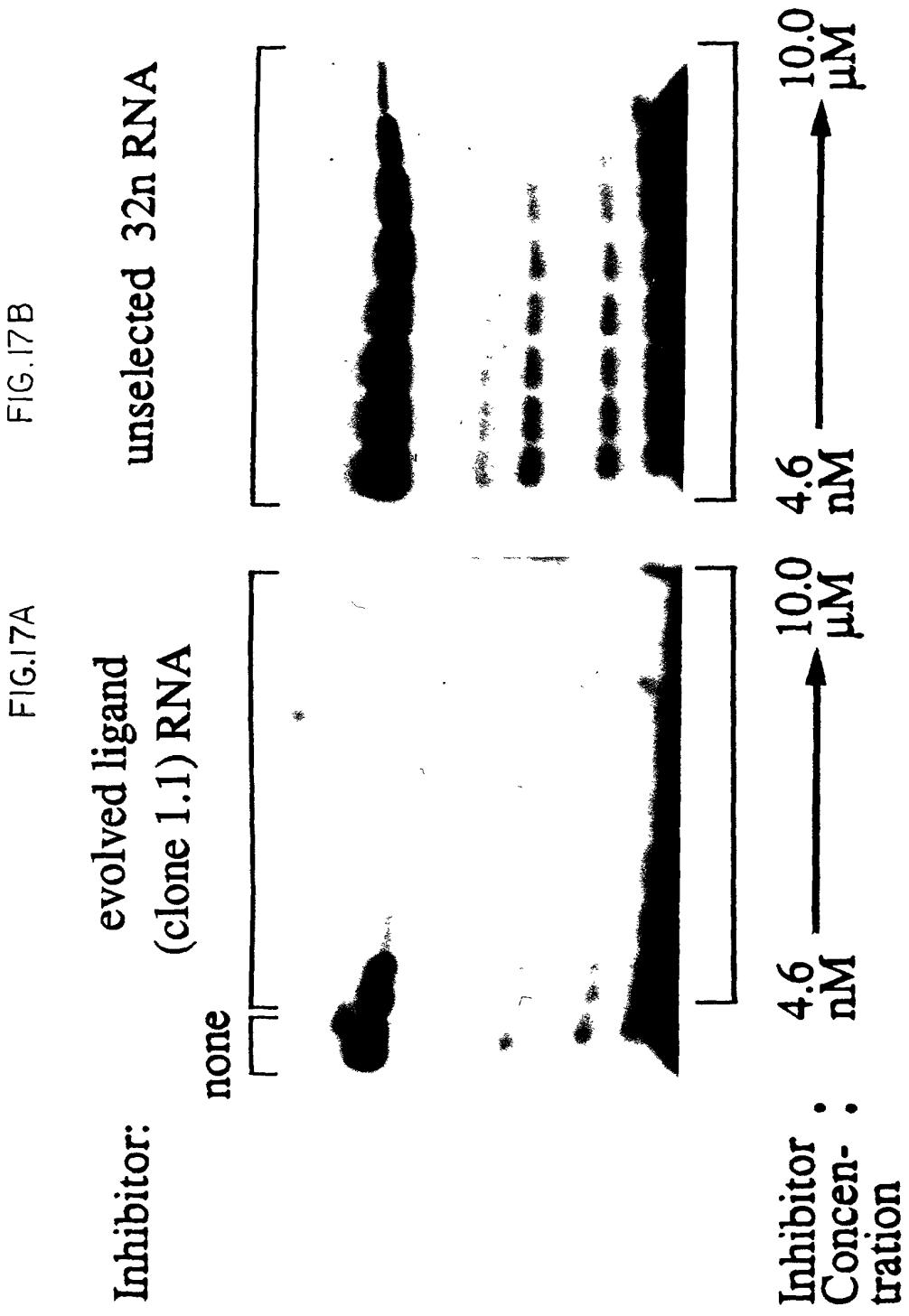


FIG.16 B

SEQ. I.D. NO. 364

FIG. 16 C





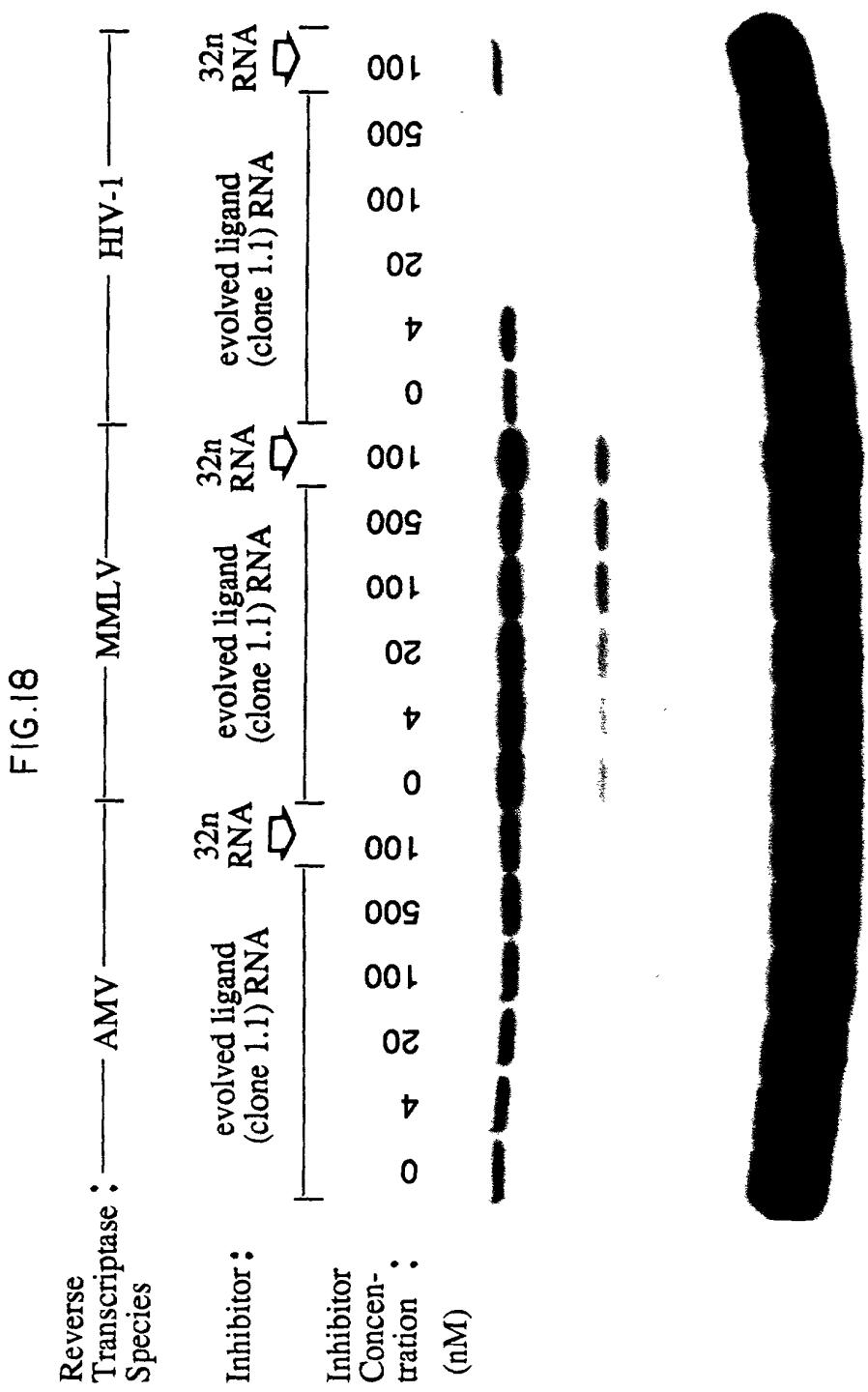


FIG.19B

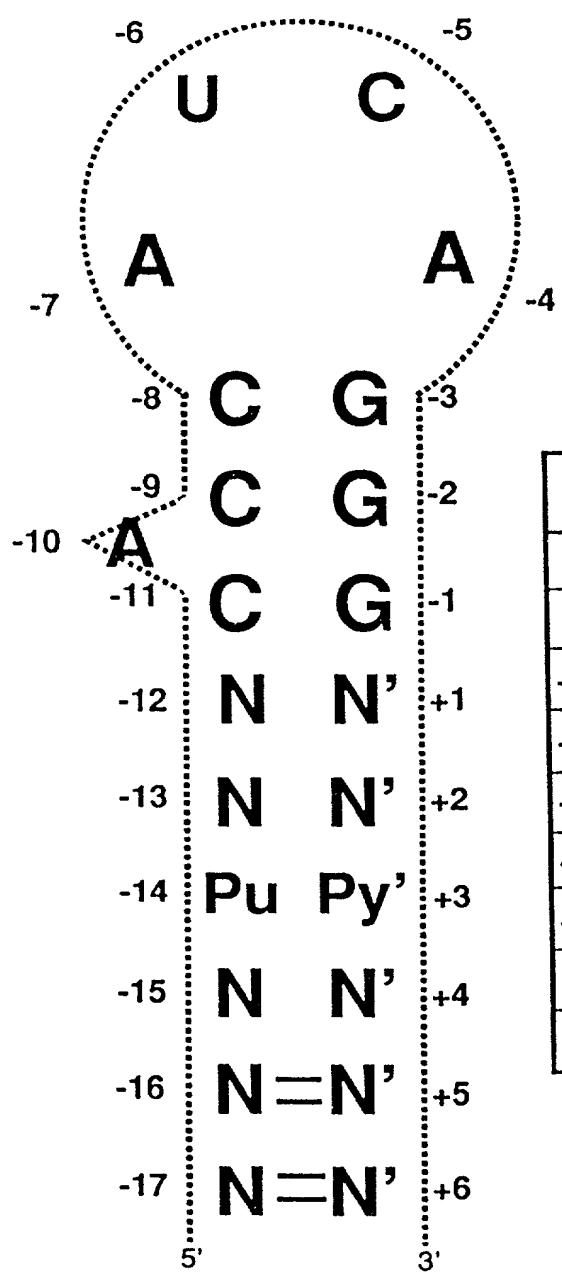


FIG.19A

SEQ. I.D. NO. 367

	A	C	G	U
-4	36	0	0	0
-5	0	36	0	0
-6	4	3	1	28
-7	36	0	0	0
-10	36	0	0	0

	AU	CG	UA	GC	UG	GU	Bulge	END
-8/-3	0	24	0	12	0	0	0	0
-9/-2	0	25	0	10	1	0	36	0
-11/-1	0	24	2	10	0	0	0	1
-12/+1	8	1	8	10	7	1	3	3
-13/+2	6	5	8	9	3	1	3	4
-14/+3	9	0	4	10	2	3	6	8
-15/+4	4	0	9	6	0	1	0	2
-16/+5	10	1	2	1	1	3	1	1
-17/+6	0	4	6	1	4	2		

FIG.19C

FIG.20

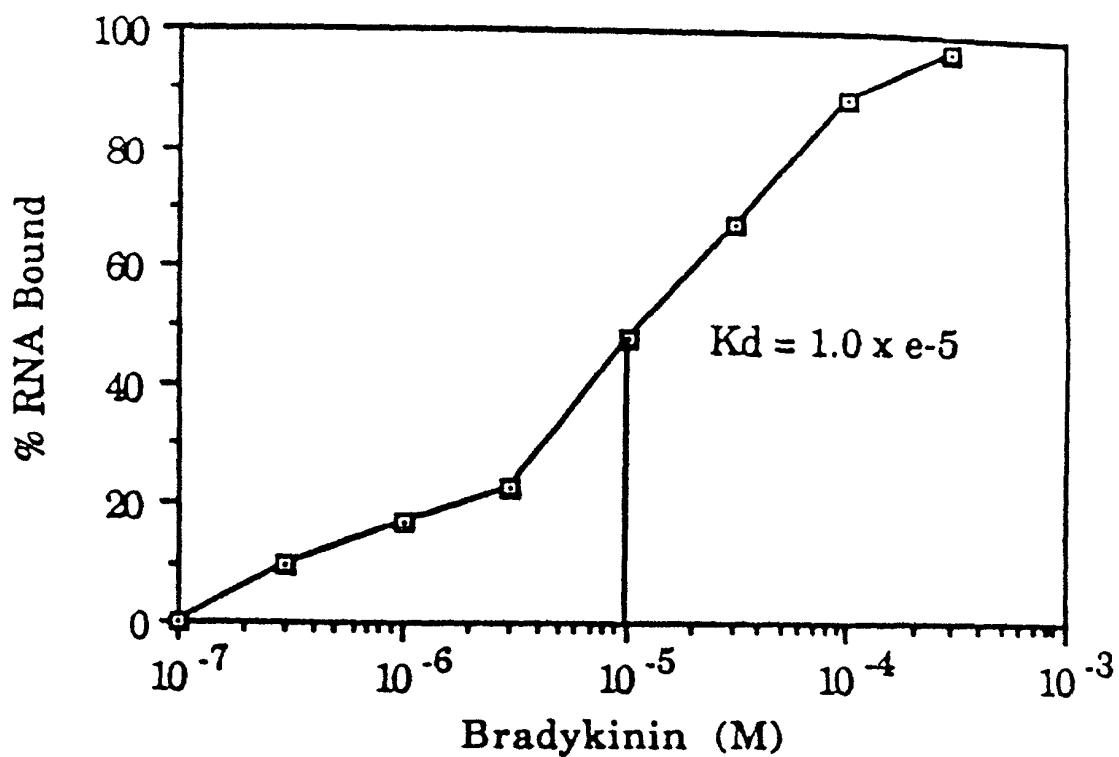


FIG.21A

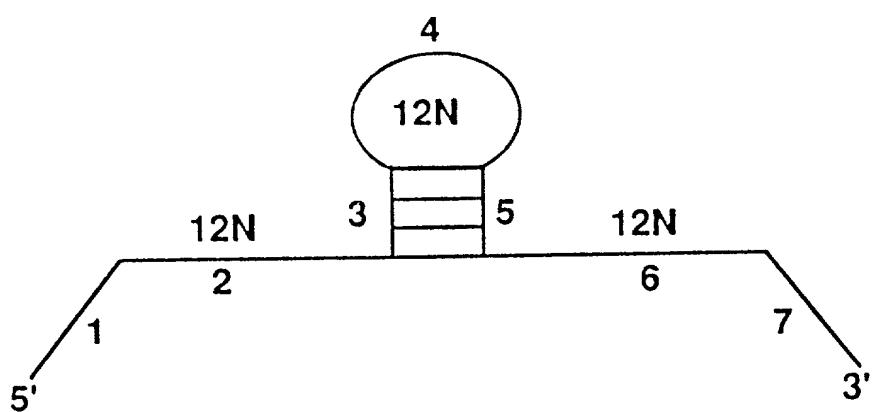
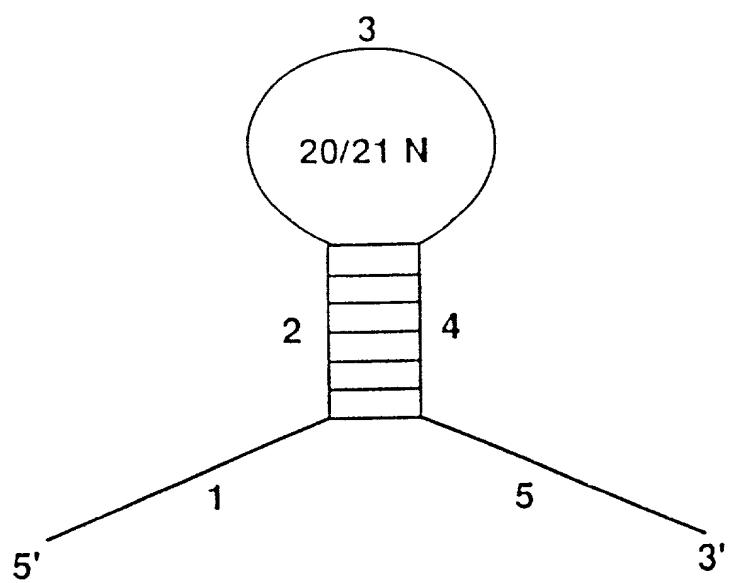


FIG.21B

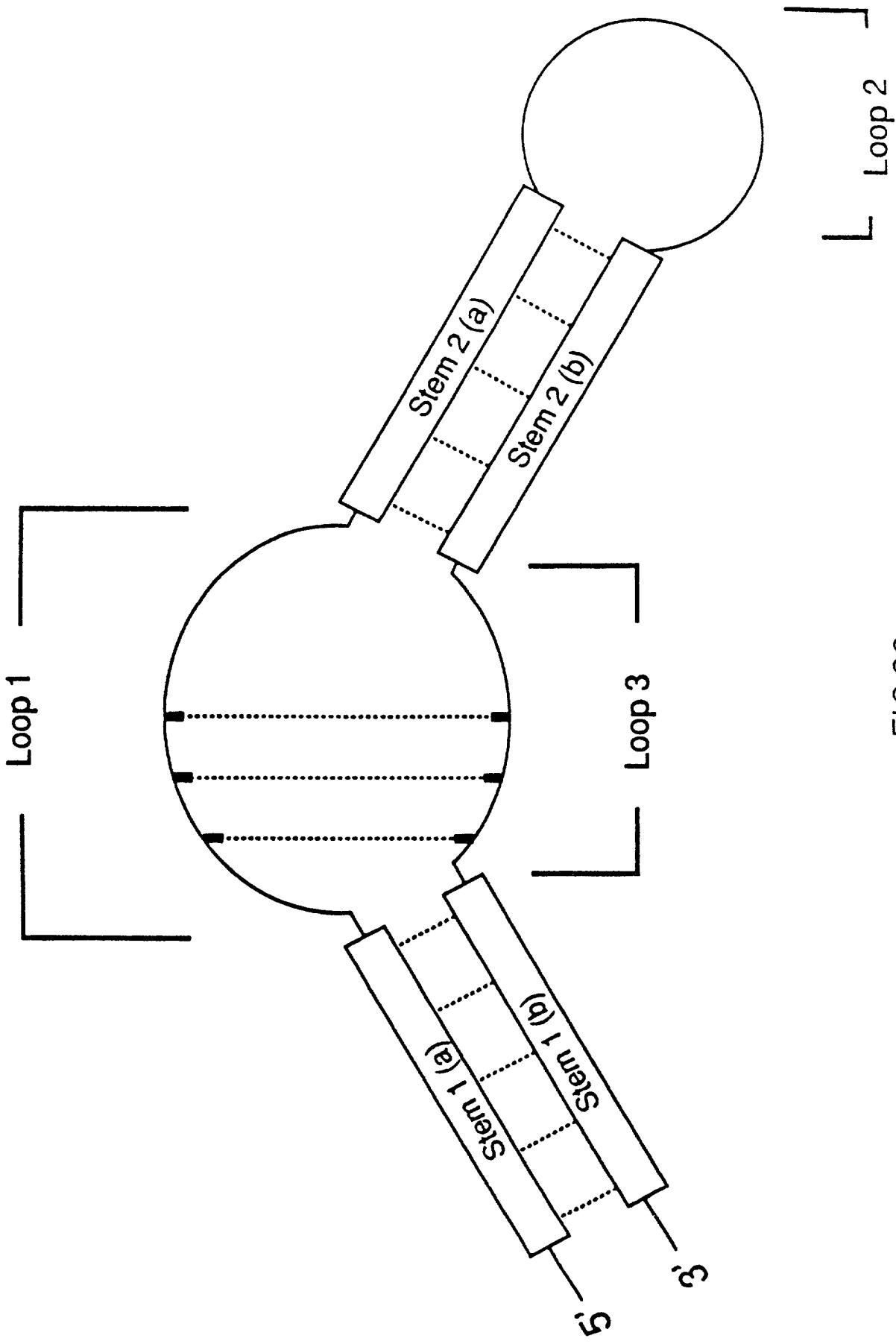


FIG.22

Motif I (6a)

UUGAGAAA G  
5' . . . gGGUGCA | | | CAC U (NUCLEOTIDES 2-38 OF SEQ. I.D. NO. 301)  
3' . . . ucuauGU | | | GUG U  
--CUCA-G U

Motif III (9a)

CC UUGaucua-  
A GG | | | ugaa-3'  
A CC | | | GCUU-5'  
UU --CUAGUAA

SEQ. I.D. NO. 369

Motif II (1c)

AAGAUAA UCU  
5' . . . AGAUG CAGC  
3' . . . ucuAC GUCG A  
-ACA-G UAG

SEQ. I.D. NO. 368

WT (Motif II-like Domain)

U ACGGUUA  
A GACGCCUG | | CA . . . 3'  
CUGGCAC | | GU . . . 5'  
A -GCCG-G

SEQ. I.D. NO. 370

FIG. 23

FIG. 24

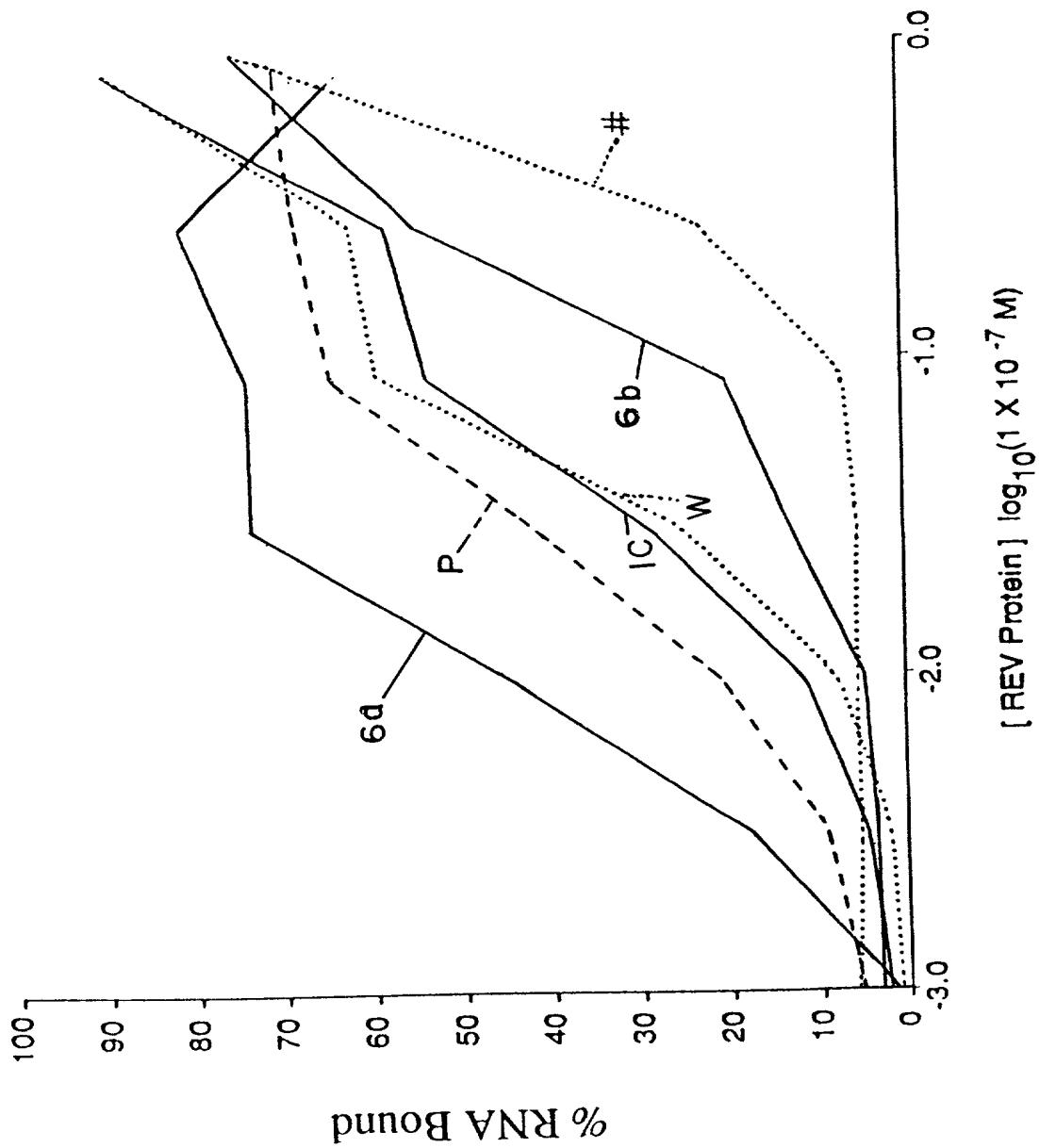


FIG. 25

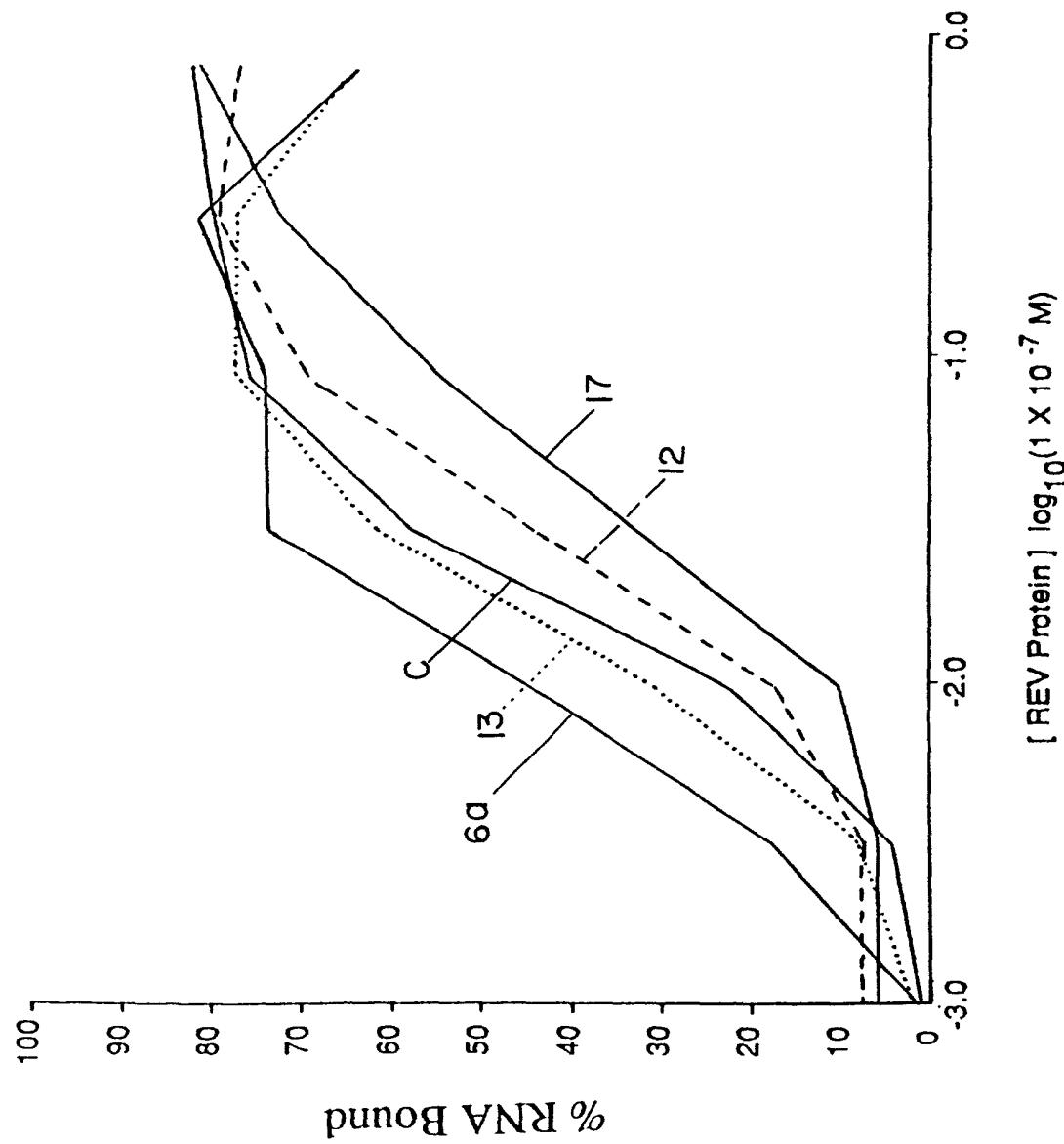


FIG. 26

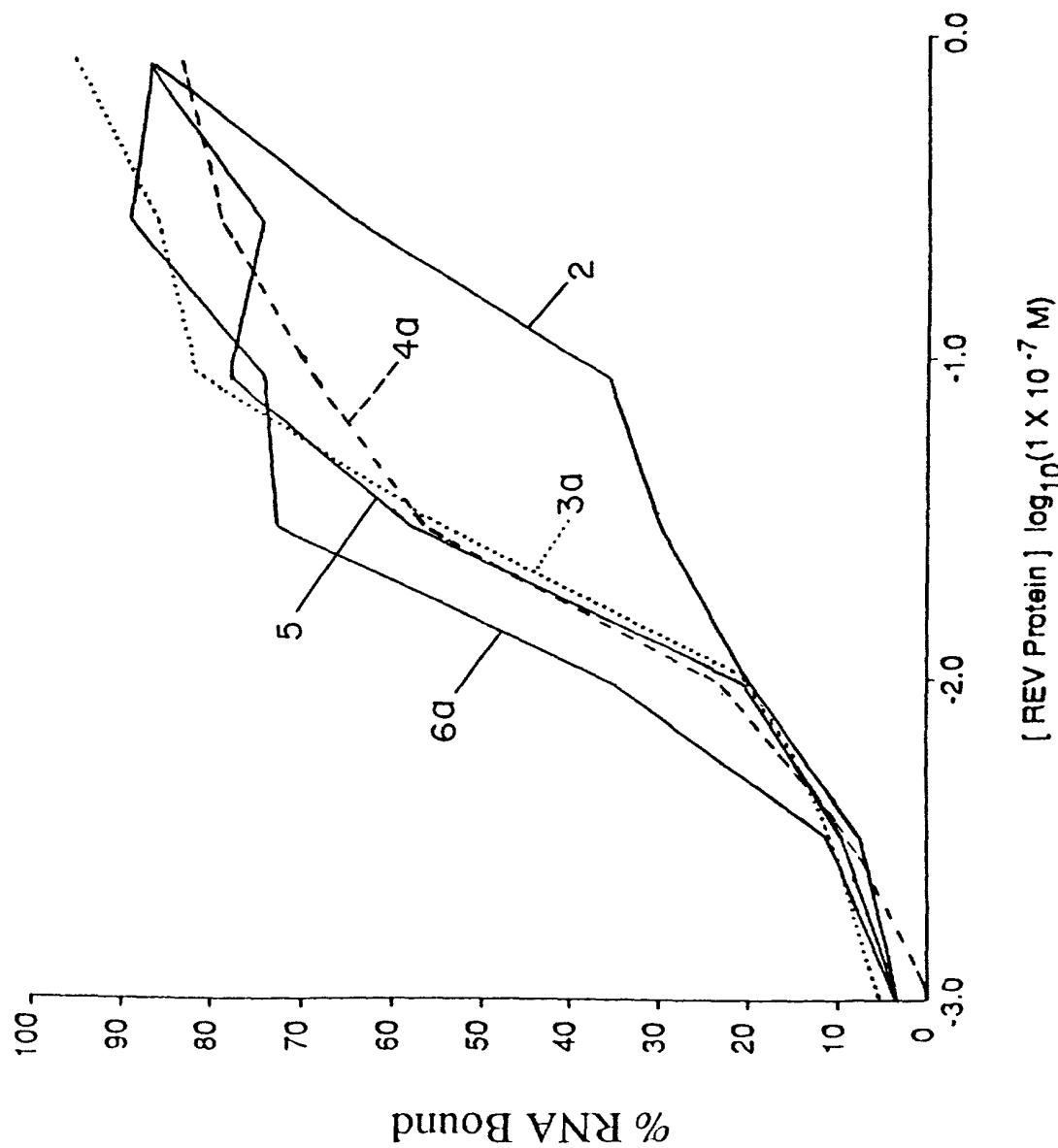


FIG. 27

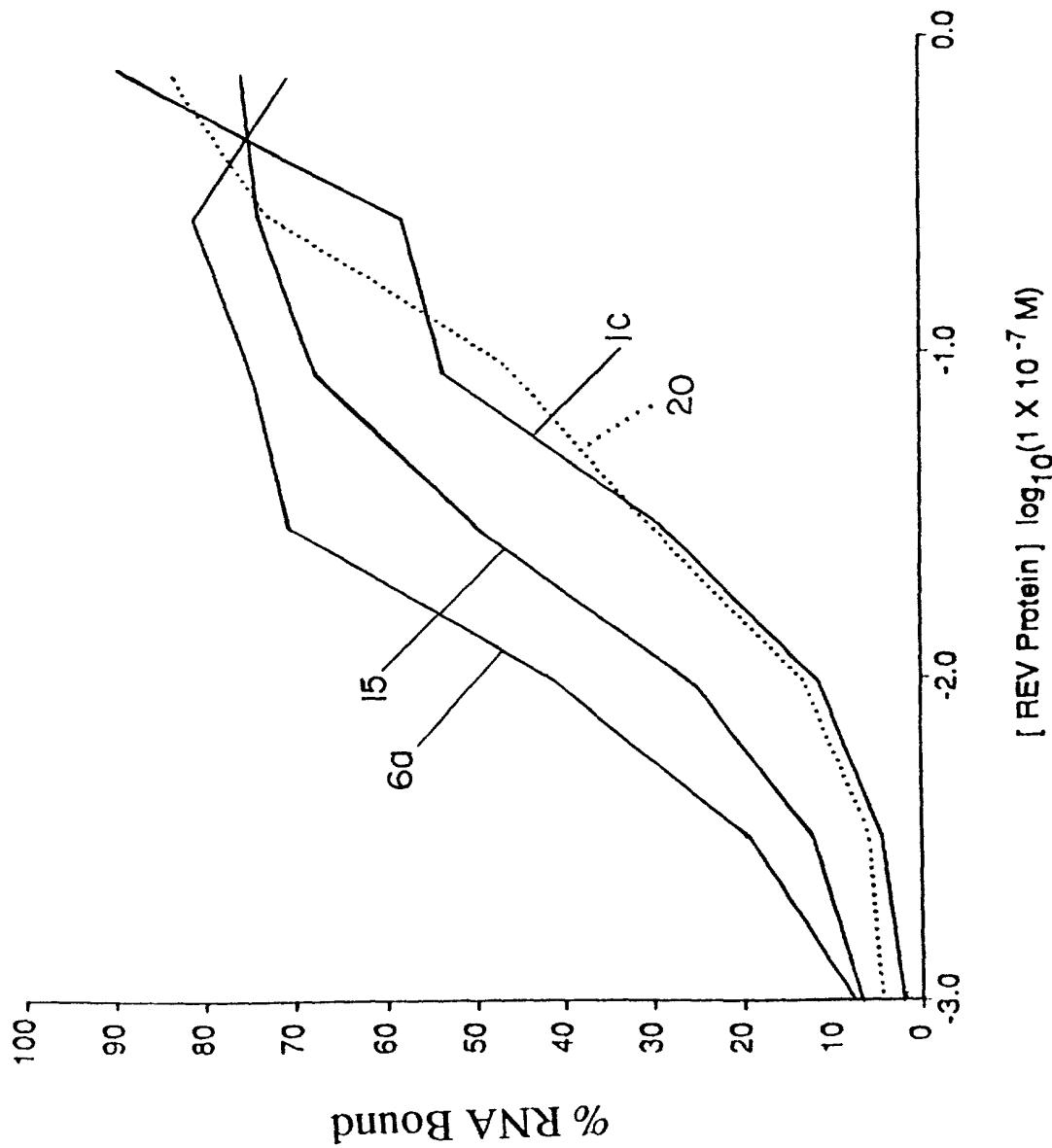
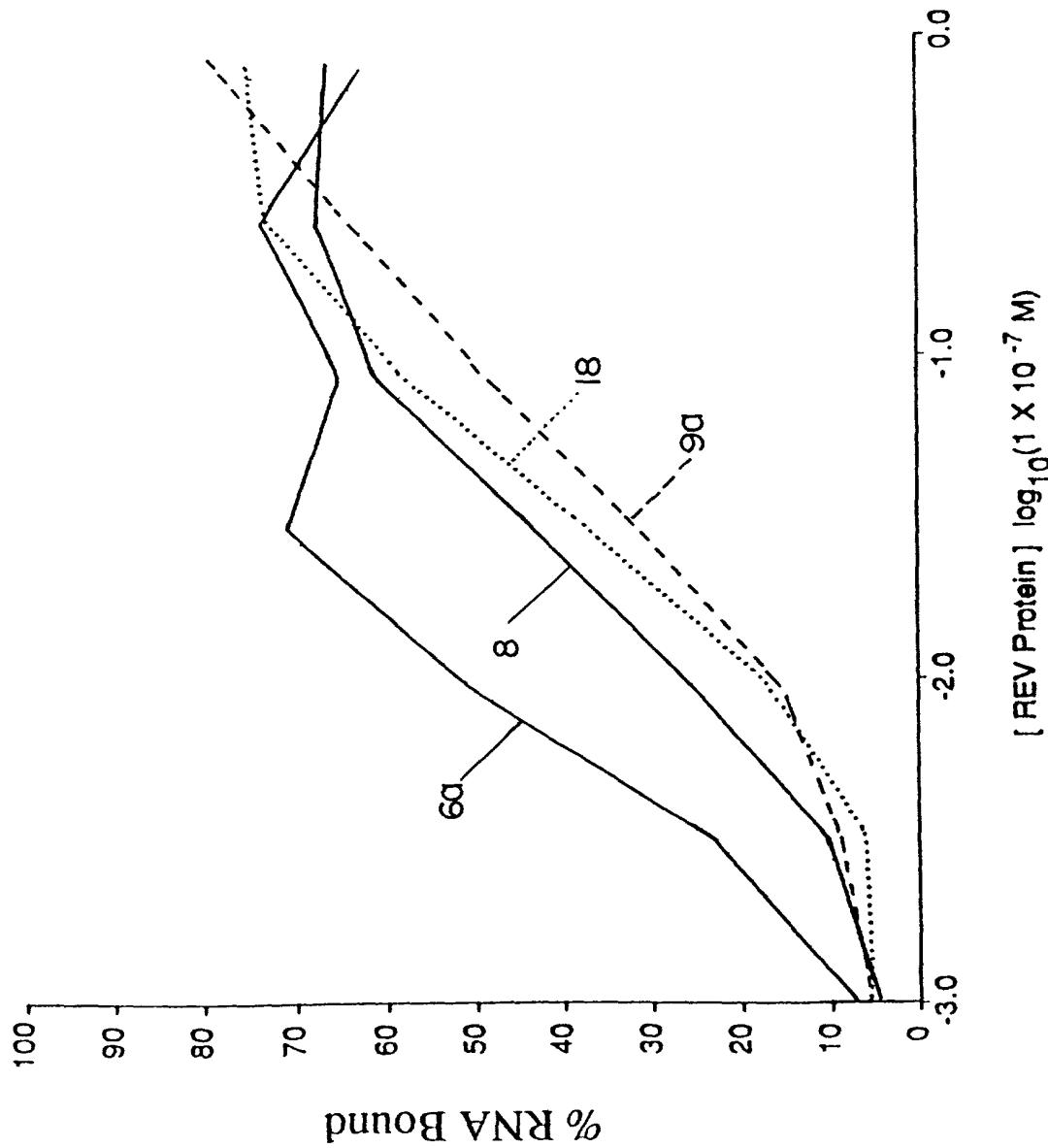


FIG. 28



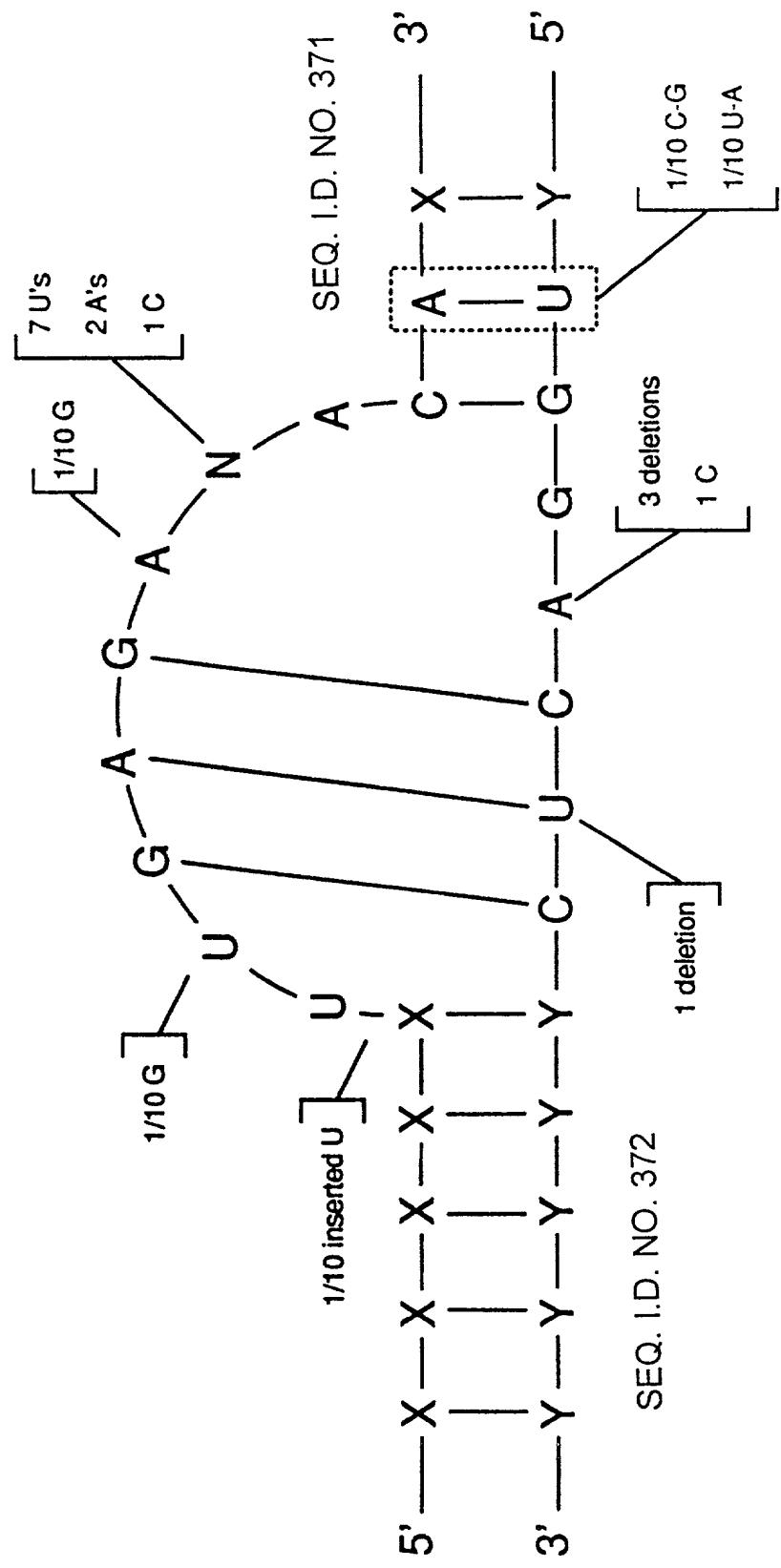
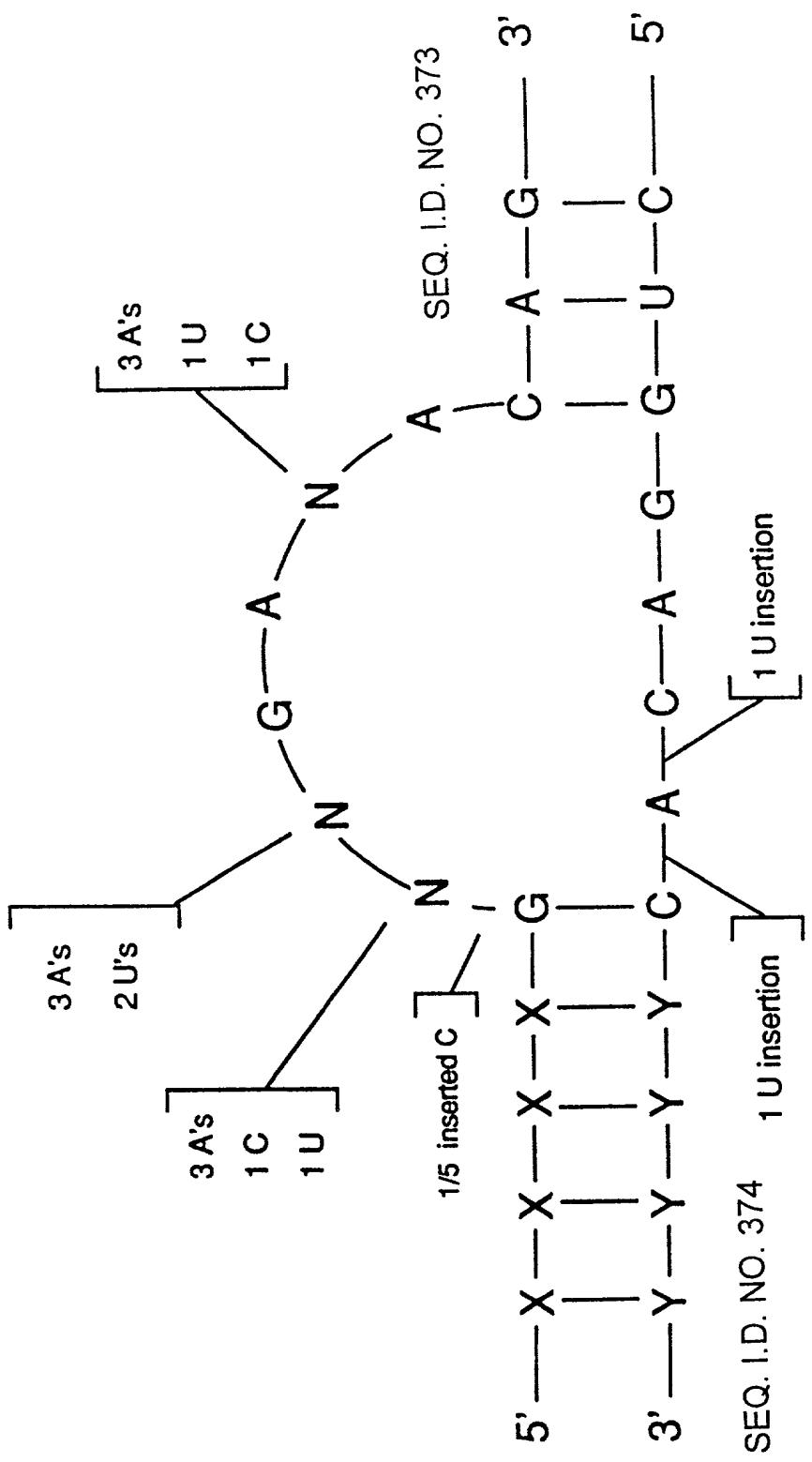


FIG. 29

FIG. 30



## Motif II

FIG. 3I

